

899

```
1 ATGGACTTCA AACAAATTGA TTTTTCACAC CTGATCAGTG TTTCCGGTTG
51 GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTGCGCGCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCCGC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC TTAAGAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCCGCTTT
551 GCGCGCCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAAGAG CGGTGTTGAA AGCCGCGCGC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```
1 MDFKQDFDLH LISVSGWGH L AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51 VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNCIDLK
201 AKEAVLKAAV EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```
1 ATGGACTTCA AACAAATTGA TTTTTCACAC CTGATCAGTG TTTCCGGTTG
51 GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTGCGCGCG
101 CGCTGCTTAT TTTTCTGGTC GGGAAATGGG CGGCGAAACG CATTGTCCGC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAGATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT
551 GCGCGCCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAAGAG CGGTGTTGAA AGCCGCGGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```
1 MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51 VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNCIDLK
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*
```

m579-1/g579-1 98.6% identity in 282 aa overlap

```
10 20 30 40 50 60
m579-1.pep MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
g579-1 MDFKQDFDLHLISVSGWGHLEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
10 20 30 40 50 60
70 80 90 100 110 120
m579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
g579-1 VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
70 80 90 100 110 120
130 140 150 160 170 180
m579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPSNVVMGNSIVNRST
```

```
|||||:
g579-1    GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||:|||||:|||||:|||||:|||||:|||||:
g579-1    LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
          |||||:|||||:|||||:|||||:|||||:|||||:
g579-1    AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```
a579-1.seq
1  ATGGACTTCA AACAATTGTA TTTTTCACAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGGTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTTGGCGGT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCGTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGCAGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GGCGTCGATT ACAATGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```
a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPNVSV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQORDIHI NS*
```

a579-1/m579-1 99.6% identity in 282 aa overlap

```
          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWA AKRIVAVMRAAMTRAQ
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1    MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWA AKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1    VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1    GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1    LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
```

```

|||||
m579-1  AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaatca gcttggtaaa gccgtgtcgc caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1  MDSPKVGCGW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATCGGGCC GGTTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCGW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

m580.pep      10      20      30      40      50      60
MDSPKVGCGWMVLPSAASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS
|||||
g580          10      20      30      40      50      60
MDSPKVGCGWMVLPSAASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS
|||||

m580.pep      70      80      90     100
QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX
|||||
g580          70      80      90     100
QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX
|||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATCGGGCC GGTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCGW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPM	SAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS				
a580	MDSPKVGCGWMVLPM	SAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS				
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1 atgcacttcg cccagcttgt gggcaaac ggtatagaac aaaatacgtt
51 ctgtcgtcgt ggttttacc gcacgatat gggcggaat accgatgttg
101 cggtagagcg tgatcggggt cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgaagga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg tttttcaac gcaccgccac ggccttcgga cgcacaaac
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgcga acccaacgca ttgcaaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTTACGAGCC ATTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTTCAAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAGRANPAHCQSQTAX					
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLLTFAGRVANPTHQCSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:


```

a581.seq
1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMG	GNTDVTVQADRG	LTSHFISLSK	LETEVRECFV		
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDM	GNTDVTVQADRG	LTSHFISLSK	LETEVRECFV		
	70	80	90	100	110	
m581.pep	GFSHTVYFFTF	FFQRTATAFG	RINQFACQTQ	VHGFLLTF	AGRIANPAHCQS	QTAX
a581	GFSHTVYFFTF	FFQRTATAFG	RINQFACQTQ	VHGFLLTF	AGRIANPAHCQS	QTAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51  agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggacgggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggtat aagggcgagg cggctattgt tgttgaaaaa ggccggggatg
251 cgcttcctgc cgacagtgcg ggcgaaaccg ccgatatcta tacgcctttg
301 agcctgatgt acgacttggg caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt acctatgcc gttttgggat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg cgcggatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttccgca atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcgat ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751 aggatttatg ccatggcagg catggaatgg ggcaaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgttaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc ggggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
1  MRYILLTGLL PTSAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPPFWY NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYDM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCTCTG CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCTTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCCGGACAG AGAACGTGC GGAACCAAAA TTGCAGGTTT CGTCAAAAG
501 CAAAATTGCC GAAGATTTGT TTAATAACCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCGA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCCTGT
651 GAAGGCGGAG TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAAATGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLDDND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDVKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYDM GYGDVKLQYR
301 LNDRONVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	70	80	90	100	110	120
	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDDNDLRGLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDDNDLRGLLGVREH					
	70	80	90	100	110	120
m582.pep	130	140	150	160	170	180
	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNSPNYAPSSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	190	200	210	220	230	240
	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	250	260	270	280	290	300
	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDMGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

```

m582.pep  LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||
g582      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1   ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTTC GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TTAAAACCCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGCG CCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1   MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLDKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDKNDLRGLLGVRH
          |||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
               130      140      150      160      170      180

               190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               190      200      210      220      230      240

               250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIDYMGYGDVKLQYR
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIDYMGYGDVKLQYR
               250      260      270      280      290      300

               310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
               310      320      330      340      350      360

               370
m582.pep      GLMFNDLDGIX
               ||||||||||
a582          GLMFNDLDGIX
               370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacgcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg caatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcat cgctcatcgc cgcgcccggg ttgtcggcgg
351 ttacgcgggt tactgcgacc aaccgcagcg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTTCGGA AGAGCGAGAC TGTAAACGAT GCCACGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TACGCGGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTORIAHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LRKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAF CGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNGSQQ	QFGKSETVTD
g583	MIIDQSQIFT	HLAFCAF CGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNGSQQ	QFGKSETVTD
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDK	QISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTORIAHR	RARFVGGYAG
g583	AQRFSKNGDK	QISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTORIAHR	RARFVGGYAG
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRLDP	VGYGQCQNQG	AQYCGNGEGY
g583	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRLDP	VGYGQCQNQG	AQYCGNGEGY
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHD	LRKKDRPEKSEKX				
g583	RFETQFHHD	LRKKDRPEKSEKX				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAT TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTGCGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTORIAHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LRKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAF CGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNGSQQ	QFGKSETVTD

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQFGKSETVTD
              10      20      30      40      50      60

              70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
              |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG
              70      80      90      100     110     120

              130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              130     140     150     160     170     180

              190     200
m583.pep  RFETQFHHIDLRRKDRPEKSEKX
              |||||
a583      RFETQFHHIDLRRKDRPEKSEKX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1   atgtctcggtt ctatcttggc ggcttcctctg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggagggca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgcgctttt gcttttcaag gcgcgtgccc aaaaactggc
501 gggcgcttctg ggtgcgtccg gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtta cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:...

```

1   MLRSILAASL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNVANA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEPK AGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1   ATGTTGCGTC TTGTTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAATTCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCATCAG
451 GTCAGCAAAG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSR SAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep    MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584         MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVAAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep    EFVKKFNKFI RSKNGSFKT ELVSR SAMPR YQYTNRRRIQTGWEERAEFKVEGRDFDELN
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584         EFVKKFNFT RSKNGSFKT ELVSR SAMPR YQYTNRRRIQTGWEERAEFKAEGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep    RFIADIQADAALXYTDFHVS RERRNEVIXQVSKDAVLRFKARA EKLAVLGASGYKIVKL
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584         RFIADVQTDASLED TDFSVSRERRNEVIDQVSKDAVLRFKARA EKLAVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep    NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584         NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKG TDSAAPGVEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGCGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGTTGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CCGATTCCGC
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSR SAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDELN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep    MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
a584         MLRSILAASL-----IVEFS ESAGVEAVQDTMSARFQVTAEGRDKNVNA
              10      20      30      40

```

	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNGRRITQGWEEAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPYQYTNGRRITQGWEEAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt tccaacgcat tttcgccaca ttttgccgcg ttatcgctctg
51  cgcaatcttt gtggcgagtt tttctttttg gctgggtgcag aacacccttg
101 ccgaaaacca attcaaccaa cgccgcacca tcgaaaccac attgatgggc
151 agcattatct ccgcattcaa gacacggggc gacaacggcg cgccgcgaaat
201 cctgaccgaa tggaaaaaca gcccgcgttc atccgcgctt tacgtcatatc
251 agggcgacga gaaaaaagac atcttaaaac gctatatcga caattacacc
301 atagaacgcg cccggctggt tggcgccaac aacccccatt ccaaccttgt
351 ccgcatcgaa tacgaccggt tcggcggaaga atacctgttc ttcattaaag
401 gctgggacaa ccaccaggca caacgcctgc ccagcccgct gtttateccg
451 ggcctgcccg ttgcccgat ttggcacgaa ttcattcatc tctccttcac
501 catcattgtc ggactgctga tggcatatat ccttgccggc aacattgcca
551 aacccatcag aatcttaggc aacggcatgg acaggggtggc agaacgagaa
601 cttgaagacc gcgtttgcca acaggttcgc gaccgcgacg acgaattggc
651 cgatgttgcc atgcaattcg acacaatggt ggaaaaactg gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFKTRG DNGAREILTE WKNSPVSSAV YVIQGDDEKQ ILNRYIDNYT
101 IERARLFAAN NPHSNLVRIE YDRFGEEYLF FIKGWDNHQA QRLPSPLFIP
151 GLPLAPIWHE FIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVAERE
201 LEDRVCQQVR DRDELADVA MQFDTMVEKL E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAACTGT TCCAACGCAT TTTGCCACA TTTTGCGCGG TTATCGTCTG
51  TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCCTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGCGGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCTGAACC GGTATATCGA CAGCTATACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGCG CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCATATAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC
651 CCATCTTGCC ATCCAATTCC ACAAAATGGT GGA AAAAATC GAAAAACTCG
701 TTGCAAAAGA ACGCCACCTG CTCCATCAGC TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAAGT ACCCGCATGG
851 ATACGCTGGC CGGGGAATG TTAACCCCTG CCCGTCTCGA AACTTCCAAT
901 TTGCTTTTGG AAAAAGAAAG CCTGAAACTG CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA

```



```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCAGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIIVG LIQAQPOKQE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
g585	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKDD ILNRYIDSYT IERARLFAAG HPHSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQGDEKDD ILNRYIDNYT IERARLFAANN HPHSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLIP GLPLAPIWHE LIILSFIIIV GLLMAYILAG					
g585	YDRFGEEYLF FIKGWDNHQAQR LPSPLFI PGLPLAPIWHE LIILSFIIIV GLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILG NGMDRVANGE LETRISQQVDDRDEL SHLAIQFDKMVEKLEKLVAKERHL					
g585	NIAKPIRILG NGMDRVAERELEDRVCCQVDRDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRS PLARMQAIIVGLIQAQPOKQE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

```

```
651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAAGAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTACCCG TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAAGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```
a585.pep
1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGEKKD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQOE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
301 MALEKESLKL LPFLGNLVED NQSI AQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*
```

m585/a585 99.8% identity in 468 aa overlap

```

      10      20      30      40      50      60
m585.pep MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG
|||||
a585      MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG
      10      20      30      40      50      60

      70      80      90      100     110     120
m585.pep DAGAREILTEWKDSPVSSGVYVIQGEKKDILNRYIDSYTIERARLFAAGHPHNSNLVHIE
|||||
a585      DAGAREILTEWKDSPVSSGVYVIQGEKKDILHRYIDSYTIERARLFAAGHPHNSNLVHIE
      70      80      90      100     110     120

      130     140     150     160     170     180
m585.pep YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
|||||
a585      YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
      130     140     150     160     170     180

      190     200     210     220     230     240
m585.pep NIAKPIRILGNMMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL
|||||
a585      NIAKPIRILGNMMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL
      190     200     210     220     230     240

      250     260     270     280     290     300
m585.pep LHHVSHEMRSPLARMQAIVG LIQAQPKQOE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
|||||
a585      LHHVSHEMRSPLARMQAIVG LIQAQPKQOE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
      250     260     270     280     290     300

      310     320     330     340     350     360
m585.pep MALEKESLKL LPFLGNLVEDNQSI AQKNGQ TVTSLADGKI PENTTILANESYLYRAFDNV
|||||
a585      MALEKESLKL LPFLGNLVEDNQSI AQKNGQ TVTSLADGKI PENTTILANESYLYRAFDNV
```

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTNNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTNNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51  ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tcggctactt gggatacacg gtttaccaaa accgtgctgc ttcccaaat
151 caggaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttccgcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcgtta cgatgttgcc gaaggctcatt tgaatatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgtc
401 tgggctgtgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctcgacacgc cggttgaggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggc tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFYFWKT TGKWLFALLI LAALGYLGYT VYQNRASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAEISKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EHLKWLNSN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151 LDFPVEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAACT TTAAATATTT
51  TTGGAACC ACAGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTACCAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT ACCCAAACCT CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 GTTGTCCAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAGAG CCAGGAAGCC TTAAAAAAT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCTG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51  QEAAAVLANI VEKAQSKAPQ SEINAEITKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EHLKWLNSN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151 LDFPVEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFYFWKTTGKWL <u>FALLI</u> LAALGYLGYTVYQNRKVSQNEAAAVLANI					

```

g586      MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAAALGYLGYTVYQNRAASQNEAAAVLANI
           10      20      30      40      50      60
m586.pep  70      80      90      100     110     120
           VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQVLSN
           70      80      90      100     110     120
m586.pep  130     140     150     160     170     180
           QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180
m586.pep  190     200     210
           LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELLQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTGGAAGAG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 ATTGTCCAAC CAAAAAGACA GCCTGATCCA GGCCTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCTCAAG ATTCTGTGG TCGCGAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLQVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

m586.pep  10      20      30      40      50      60
           MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYT VYQNRAASQN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYT VYQNRAASQN
           10      20      30      40      50      60
m586.pep  70      80      90      100     110     120
           VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQVLSN
           70      80      90      100     110     120
m586.pep  130     140     150     160     170     180
           QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

```

915

	190	200	210
m586.pep	LKNYGQALEKMPQDSVGREL	VQMKLDSLKX	
a586	LKNYGQALEKMPQDSVGREL	VQMKLDSLKX	
	190	200	210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgccc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggg ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaaactc acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGCTG
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

```

m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
                |||||||||||||||:|||||||||||||||||||||||||||||:| |||||||
g587          MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
                10          20          30          40          50          60

                70          80          90          100         110         120
m587.pep      TGATSFIPIPTEIQENGSNNDMLVGLTGLRYGLTGNTDIYGSGSYLWHEERKLDGNSKTR
                |||||||||||||||:|||||||||||||||||||||||||||||:| |||||||
g587          TGATSFIPIPTEIQENGSNNDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR
                70          80          90          100         110         120

                130         140         150         160         170         180
m587.pep      NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:| ||||||| ||||||| ||||||| |||||||
g587          NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKRRGLCPFFYNLRINYEY
                130         140         150         160         170         180

                190         200         210         220         230         240
m587.pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRDTGK
g587          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GTGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCCG
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCGT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGAGT ATCCCTCGG ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGAGC GCAATTACTG GATGCTGAAT CCAATATAT CTTTCGCGCG
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACACCGG CTTTAAACGC
801 ATCCGACGCT TTCACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTTA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

a587.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSENNRR
51	AELAAPVYIQ	TGATSFPIIP	TEIQENGST	DMLVGTGLGR	YGLTGNTDIY
101	GSQSYLWHEE	RKLDGNGKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKADIPVV	LSLTAAYRIN	GSKTLLSNTK
201	YKAGNYWMLN	PNISFGAANDR	ISLTGGIQWL	GKQPDRLDGK	KESARNTSTY
251	AHFGAGFGFT	KTTALNASAR	FNVSQSSSE	LKFGVQHTF*	

m587/a587 95.2% identity in 289 aa overlap

```

      10      20      30      40      50      60
m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAEAAPVYIQ
          |||||:|||||
a587      MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAEAAPVYIQ
          10      20      30      40      50      60

      70      80      90     100     110     120
m587.pep  TGATSFIPIPTEIQENGSDMLVGLTGLRYGLTGNTDIYSGSGSYLWHEERKLDGNSKTR
          |||||:|||||
a587      TGATSFIPIPTEIQENGSDMLVGLTGLRYGLTGNTDIYSGSGSYLWHEERKLDGNGKTR
          70      80      90     100     110     120

```

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
  1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
 51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101  aaggcgggat cggaagac gggcttcctt caggcaaagg catatggcgt
151  tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201  cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251  cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301  ttcaaacaag gcttggcaca cggcagggtc gccgcctcgc aaaacggcga
351  aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
  1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
 51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101  FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
  1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
 51  CACTTCGGCC GCCGTCCTGA CTTCTATCA AGAACCAGGC TGCACCTACG
101  ACGGCAATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151  TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAACG GCAAATTCGA
201  CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251  CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301  TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351  AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401  TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
  1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
 51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101  FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPHKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep      MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVVGKDGPAGKGTWRCQDGRNYTGS
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g588           MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDLPSGKGIWRCRDGRGYTGS
               10      20      30      40      50      60

               70      80      90      100     110     120
m588.pep      FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:
g588           FKNGKFDGQGVYTVAAAGREVLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
               70      80      90      100     110     120

               130     139
m588.pep      IMKCENGMIKEVKLPKNKX
g588           YYEMRTRHDX
               130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CGCCGCGTCC GCCGTCTCTGA CTTCCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1   MLKHLAFLLP AMMFALPAAS AVLTYSYQEPG CTYEGDVGKD GKPAGKGTWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

```

m588/a588 96.4% identity in 138 aa overlap

```

               10      20      30      40      50      60
m588.pep      MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVVGKDGPAGKGTWRCQDGRNYTGS
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a588           MLKHLAFLLPAMMFALPAASAVLTYSYQEPGCTYEGDVGKDGPAGKGTWRCQDGRNYTGS
               10      20      30      40      50      60

               70      80      90      100     110     120
m588.pep      FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a588           FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               70      80      90      100     110     120

               130     139
m588.pep      IMKCENGMIKEVKLPKNKX
               |||||
a588           IMKCENGMIKEVKLPKNKX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1   atgcaacaaa aaatccggtt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tggtgaacaa aaaagatttt gtcgaatcgg
101 cgggagttaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```



```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgcAAC
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgtcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg ggcacggta
551 tggcgcatgt gtattttgaa gcgggcgtga tggatgatcg ttttgtgtcg
601 ctgggtaagt ttttggaaaca ccgcaccaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaacg catcgctgcc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggc
901 agcgtggtgt accgcgcgcg gcagctcgcc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagttaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggctg attaaggcgg attggacggg
1101 cgcactgatg cacgcctgtg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggctctggc gacccttgcc gcgattatgg tcggcatggg caaagcgggt
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgccgtttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgccg cccaccgcgt
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccc
1451 ctgcacaaaa tgcgcaaacg gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaaccc atcggcgcat tcgcaacttc cgacgcgttg
1651 aaagccgata ccgcccgaag cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtcc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaacccg tggcgatggg
1851 cggcgacggc atcaacgacg gcgccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcggtt tcgggtatttg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

```

g589.pep..
1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPI YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSWG ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAI PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRFPQVAAY YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

```

m589.seq..
1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTG TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTT

```

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CCGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCCTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AAGCCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGC GCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTGCTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTTAAACA CCGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGCTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCCACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCAAC
1451 AAACCGTTGT CCGCGCAGGC ATTACCGCG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TGCGGTCTCA GTCGATAACA
1601 AACCACATCG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CCGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CCGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCCTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TCGCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCC
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTTC
2051 CTCTCGCCGC GCTTGGCTTT TAAATCCCG TCATCGCTGG CGCGGCAATG
2101 CGGGCAAGCT CGGTTTCCGT GTTGAAGCAAT GCCTTGCGCC TGAACCGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLFTINVFPFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251 ERIAADGIIE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVEVP AVVGIALLTFF
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEAA AHVDAVVLDA TGTLTGEGSPQ VAAVYCVFDS GFEDDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

              10          20          30          40          50          60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANKI
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
	:					
g589	EIPAAQNAQTVVGAGITAEEVGVGLVKSGKAFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
	:					
g589	IGAFALSDALKADTAEAIIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
	:					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCCCTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGCGCA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCGTATATCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAAAC CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAATCA CGCCAACCCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAAATCGG CGACCTAATC
751 CGCGCAATC ACGGCGAAGC CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCAGAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGCGCG GCGCGTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCCA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCG TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATCGC TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

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923

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTGCGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCGCTC GCCGCGCTCG GCTTTTAAA CCGCGTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
  1  MQQKVRFOIE GMTQACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
 51  KTSVADIARI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101  IGMVGMMLKG LNWTRHDWML SPLLOFALAS VVQLWLAVPF YKSAWASIKG
151  GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVHYFE VGIMVIGFVS
201  LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251  RANHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301  SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVEFPAVVGI
351  ALLTFIATWL IKGDWTLALM HAVAVLVIAI PCALGLATPA AIMVGMGKAV
401  KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPQVAAYV CVPDSGFDED
451  ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501  KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551  KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601  AAEVQKLKAA GKTVMAMVDG INDAPALAAA NVSFAMKGGA DVAEHTASAT
651  LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701  AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

              10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTTSVADIARI
              ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589           MQQKVRFOIEGMTQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTTSVADIARI
              10      20      30      40      50      60

              70      80      90     100     110
m589.pep      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG----RHDWMI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589           IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMLKGLNWTRHDWML
              70      80      90     100     110     120

              120     130     140     150     160     170
m589.pep      PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
              || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589           SPLLOFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
              130     140     150     160     170     180

              180     190     200     210     220     230
m589.pep      AYGMHVHYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589           AYGMHVHYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
              190     200     210     220     230     240

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924

	240	250	260	270	280	290
m589.pep	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
	300	310	320	330	340	350
m589.pep	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VP	PAVVGIALLT	FI	VTWL
a589	SVVYRAAQLGSQTLLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VP	PAVVGIALLT	FI	VTWL
	310	320	330	340	350	360
	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA	CPCALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAAHVDA			
a589	IKGDWTLALMHAVAVLVIA	CPCALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAAHVDA			
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTGSPQVA	AVYCVDPDSGFDE	DALYRIAAVEQNAAHPLA	RAIVSAAQARGL		
a589	VVLDKTGTLTGSKPQVA	AVYCVDPDSGFDE	DALYRIAAVEQNAAHPLA	RAIVSAAQARGL		
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAE	VEGVGLVKAGKAEFAELAL	PKFLDGVWDIASIVAVS	VDNKP		
a589	EIPTAQNQITIVGAGITAE	VKGAGLVKAGKAEFAELT	LPKFS	SDGVWEIASVAVSVNGKP		
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAE	AIGRLKKNIDVYIMSGDN	QGTVEYVAKQLGIAHAF	GNMSPRDK		
a589	IGAFALADALKADTAE	AIGRLKKNIDVYIMSGDN	QGTVEYVAKQLGIAHAF	GNMSPRDK		
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKT	VAMVGDGINDAPALAAAN	VSFAMKGGADVAEHTASAT	LMQHSVNQLA		
a589	AAEVQKLKAAGKT	VAMVGDGINDAPALAAAN	VSFAMKGGADVAEHTASAT	LMQHSVNQLA		
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNL	FFAFFYNILGIPLAALGFL	NPVIAGAAMAASSVSVLS	NALRLK		
a589	DALSVSRATLKNIKQNL	FFAFFYNILGIPLAALGFL	NPVIAGAAMAASSVSVLS	NALRLK		
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:
g590.seq..

```

1  atgaaaaaac ctttgatttc agttgctgca gtattgctcg gcggttgcttt
51  ggggtacacct tattatttgg gtgtcaaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccagc
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgccctgaa acggaaaaag ttttggaacg ctttttggg aaacaagtc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

```

```

501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcy cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaat gaacgaactg
751 gtcaacctgc ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaaaaaatac ggcccgtg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgccc cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaataattg
1151 atgtgggccc aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattggggc tgatgtttaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttggcggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacgggcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacy ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGKAEES LTQOQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 YAGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM PKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSUNAED EAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGGCGTACAT TGAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAAGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTTGA TTCGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCTGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAAATCCG TATTGGACAT
951 TAAACTTTT CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGCGAAGG AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep..(partial)

```
1  ..WFTSMETTVI RLKPELLNNA RKYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE PKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSV
101 AFDYEEELSGI XLHWEXLTGE TVYQKGFKSY RNGYDAPLFK IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT EQRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL
351 MLKKTEADIR MSIPOKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT L NGDQIDTAIS LKNNQLKLNK KTLQNEPEPD
451 FDEGGMVSEP QQ*
```

m590 / g590 93.1% identity in 462 aa overlap

```

                                     10      20      30
m590.pep                          WFTSMETTIVIRLKPELLNNARKYLPDNLKT
g590                               ||||| ||||| ||||| ||||| ||||| |||||
                                     30      40      50      60      70      80
VKAESLSTQQQKILQKTGFLTVESHQYDRGWFTSTETTIVIRLKPELLHNAQKYLPDNLKI

                                     40      50      60      70      80      90
m590.pep  VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
g590       VLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                     90     100     110     120     130     140

                                     100     110     120     130     140     150
m590.pep  GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
g590       GSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKGFKSYRNSYDAPLFKIKLADKGDAA
                                     150     160     170     180     190     200

                                     160     170     180     190     200     210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
g590       FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                     210     220     230     240     250     260

                                     220     230     240     250     260     270
m590.pep  PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
g590       PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA
                                     270     280     290     300     310     320

                                     280     290     300     310     320     330
m590.pep  SALTVLKRKFAQISAKKMTTEEQRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
g590       SALTVLKRKFAQISAKKMTTEEQRNDLIAAVKGASGLFTHDPVLNLIKIFRFTLPQGKID
                                     330     340     350     360     370     380

                                     340     350     360     370     380     390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPOKMLEDLAVSQAGNIFSVNAEDEAEG
g590       VGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPOKMLEDLAVSQAGNIFSVNAEDEAEG
                                     390     400     410     420     430     440

                                     400     410     420     430     440     450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTLDGNDQIDTAISLKNQKLKNGKTLQNEPEPD
g590       RASIADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNQKLKNGKTLQNEPD
                                     450     460     470     480     490     500

                                     460
m590.pep  FDEGGMVS-EPQQX
g590       FDEGDMVSGQPHX
                                     510
```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTCCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTTGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTC GATTTCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGT
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTCAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CTTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE AGFLTVESHQ
51  YERGWFTSTE TTVIRLKPPEL LHNAQKYLDP NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNNQL KLNKGTQLQNE
501 PEPDFDEGGM VSEPPQ*
```

m590/a590 97.8% identity in 462 aa overlap

```
m590.pep
10 20 30
WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
|||||

a590
30 40 50 60 70 80
VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTIVIRLKPPELLHNAQKYLDPDNLKT

40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||

a590
90 100 110 120 130 140
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN

100 110 120 130 140 150
m590.pep
GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```

```
|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGOFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGOFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPSPGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAE
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAE
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPPQX
          |||||
a590      FDEGGMVSEPPQX
          510
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCGC GATTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTATTTTTC ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTC CGCCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCAATTC GATTGCGGAA CTTCAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGCGCA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGAAGTTTCA CCAACAATCC
1101 CGTATTGGAC ATTAATAACTT TCCGATTACG GCTGCCATCG GGAATAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
```

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```

1 MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE TGFLTVESHQ
51 YERGWFSTME TTVIRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTOAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNLNGDQID TAISLKNQNL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*

```

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFSTME					
g590	MKKPLISVAAVLLGVALGTPYYLGVKAEESLTQQQKILQKTGFLTVESHQYDRGWFTSTE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTOAYIETEFKYAPE					
g590	TTVIRLKPELLHNAQKYLPDNLKIVLEQPVTLVNHITHGPFAGGFGTOAHIEEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNNGSIAPSKIEVGKLAFASTKTGESGAFINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNNGSIAPSKIEVGKLAFASTKTGESGAFIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHDPVLNIKIFRFTLPQGKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQID					
g590	MLEDLAVSQAGNIFSVNAEDEAEARASDIADINETLRLMVDSTVQSMAREKYLTLDGNQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQNLKNGKTLQNEPEPDFDEGGMVS-EPQQX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

1	TTGCAAACCC	TTCTAGCTTT	TATCTTCGCC	ATCCTGATT	TGGTCAGCCT
51	GCACGAATTC	GGACACTACA	TCGTCGCCAG	GTTTGCGGC	GTCAAGGTTG
101	TGCGTTTTTC	CGTCGGCTTC	GGCAAACCGT	TTTTCAACCG	AAAGCGCGGC
151	GACACCGAAT	GGTGCCTCGC	CCCGATTCCG	TTGGGCGGCT	ACGTCAAAT
201	GGTCGATACG	CGCGAAGGCG	AAGTCAGATA	AGCCGATTTA	CCCTACGCTT
251	TTGACAAACA	ACACCCGCC	AAGCATCATC	CCATCGTCGC	CGCCGGTCCG
301	CTGACCAACC	TCGCActggc	ggTTTTGCTG	TACGGACTGa	gcTttctctt
351	cggcgtaaCC	GAATGCGGC	Cctatgtcgg	cacagtcgaA	cccgacaccg

```

401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGCGCGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTcAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRGR
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFGLLALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCGCGC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCC CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTC AAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGCGCGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTcAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51 DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIAARAGF QSGDKIQSVN
151 GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMAVAFFND VTRLLG*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
	70	80	90	100	110	120
m591.pep	LGGYVKMVD	TREGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
g591	LGGYVKMVD	TREGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
	130	140	150	160	170	180
m591.pep	ELRPYVGTV	EPDTIAARAGF	QSGDKIQSVN	GTPVADWGSA	QTEIVLNLEA	GKVAVGVQTA
g591	ELRPYVGTV	EPDTVAARTG	FQSGDKIQSVN	GVSQDWSA	QTEIVLNLEA	GKVAVGVQTA
	190	200	210	220	230	240
m591.pep	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
g591	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
	250	260	270	280	290	300
m591.pep	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASWQ	EWANLTRQSP	GKKITLTYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
	310	320	330	340	350	360
m591.pep	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
	370	380	390	400	410	420
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTVIEWIRG	KPLGERVQNI
	430	440				
m591.pep	GLRFGALMM	LMMAVAFFND	VTRLLGX			
g591	GLRFGALMM	LMAAAFFND	VTRLLGX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:
a591.seq

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTCTCG CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTCGACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGACACCCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGCGCT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT GGCAGTGGT AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAACATC GGTTTGCGCT TCGGCTTGC CCTCATGATG CTGATGATG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNL L PVPVLDGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMMVAFFND VTRLIC*

```

m591/a591 99.6% identity in 446 aa overlap

```

              10      20      30      40      50      60
m591.pep      LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG DTEWCLAPIP
              |||||||
a591           LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG DTEWCLAPIP
              10      20      30      40      50      60

              70      80      90     100     110     120
m591.pep      LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
              |||||||
a591           LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
              70      80      90     100     110     120

              130     140     150     160     170     180
m591.pep      ELRPYVGTVE PDTIAARAGF QSGDKIQSVN GTPVADWGS AQTEIVLNLEA GKVAVGVQTA
              |||||||
a591           ELRPYVGTVE PDTIAARAGF QSGDKIQSVN GTPVADWGS AQTEIVLNLEA GKVAVGVQTA
              130     140     150     160     170     180

              190     200     210     220     230     240
m591.pep      SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGL KPGDRLTA
              |||||||
a591           SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGL KPGDRLTA
              190     200     210     220     230     240

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	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVVISLGLVNLPLVPVLDGGHLLVIFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGLVNLPLVPVLDGGHLLVIFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg  acgtgttcgg  tcagattttt  tcggggcgcgt  tcaaattcga
51  cgcggcagca  ggcggccttac  tcggcggctct  gatttcgcaa  acgatgatga
101 tgggcatcaa  acgcggcctg  tattccaacg  aggcgggtat  gggttccgcg
151 ccgaacgcgc  ccggcgccgc  cgaagtgaag  caccctgttt  cgcaaggtat
201 gattcaaatg  ctgggcgtgt  ttgtcgatac  catcatcggt  tgttcttgca
251 ccgccttcat  catcttgatt  taccaacagc  cttatggcga  tttgagcggt
301 gcggcgctga  cgcaggcggc  gattgtcagc  caagtggggc  aatggggcgc
351 ggggtttcct  gccgtcatcc  tgtttatggt  tgccctttcc  accgttatcg
401 gcaactatgc  ctatgccgag  tccaacgtcc  aattcatcaa  aagccattgg
451 ctgattaccg  ccgttttccg  tatgctggtt  ttggcgtggg  tctatttcgg
501 cgcggttgcc  aatgtgcctt  tggctctggg  tatggcggat  atggcgatgg
551 gcacatcgcc  gtggatcaac  ctgctcgcca  tcctgctgct  ctgcgccattg
601 gcgtttatgc  tgctgcgcga  ttacaccgcc  aagctgaaaa  tgggcaaaaga
651 ccccgagttc  aaactttccg  aacatccggg  cctgaaacgc  cgcacataat
701 ccgatgtttg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF  SGAFKFDAAA  GLLGLGISQ  TMMGIKRL  YSNEAGMGSA
51  PNAAAAAEVK  HPVSQGMIM  LGVFVDIIV  CSCTAFILI  YQQPYGDLG
101 AALTQAAIVS  QVGWAGAGFL  AVILFMFAFS  TVIGNYAYAE  SNVQFIKSHW
151 LITAVFRMLV  LAWVYFGAVA  NVPLVDMAD  MAMGIMAWIN  LVAILLLSPL
201 AFMLLRDYTA  KLKMGKDFEF  KLSEHPGLKR  RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG  ACGTGTTCGG  TCAGATTTTT  TCGGGCGCGT  TCAAATTCGA
51  CGCGGCAGCA  GCGCGCTTAC  TCGGCGGTCT  GATTTCGCAA  ACGATGATGA
101 TGGGCATCAA  ACGCGGCCTG  TATTCCAACG  AGGCGGGTAT  GGGTTCCGCG
151 CCGAACGCCG  CCGCGCCCGC  CGAAGTGAAA  CACCCTGTTT  CGCAAGGTAT
201 GATTCAAATG  CTGGGCGTGT  TTGTCGATAC  CATCATCGTT  TGTCTTGCA
251 CCGCCTTCAT  CATCTTGATT  TACCAACAGC  CTTACGGCGA  TTTGAGCGGT
301 GCGGCGCTGA  CGCAGGCGGC  GATTGTCAGC  CAAGTGGGGC  AATGGGGCGC
351 GGGCTTCCTC  GCCGTCATCC  TGTATTGTT  TGCTTTTCC  ACCGTTATCG
401 GCAACTATGC  CTATGCCGAG  TCCAACGTCC  AATTCATCAA  AAGCCATTGG
451 CTGATTACCG  CCGTTTCCG  TATGCTGTT  TTGGCGTGGG  TCTATTTCCG
501 CGCGGTTGCC  AATGTGCCTT  TGGTCTGGGA  TATGGCGGAT  ATGGCGATGG
551 GCATTATGGC  GTGGATCAAC  CTGTGCGCA  TCCTGCTGCT  CTCGCCCTTG

```


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601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGLGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAEVK HPVSQGM IQM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

m592.pep	10	20	30	40	50	60
	MIPDVFGQIFSGAFKFDAAAGLLGLISQTMMGIKRG LYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGLISQTMMGIKRG LYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
m592.pep	70	80	90	100	110	120
	HPVSQGM IQMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVS QVGQWGAGFL					
g592	HPVSQGM IQMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVS QVGQWGAGFL					
	70	80	90	100	110	120
m592.pep	130	140	150	160	170	180
	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
m592.pep	190	200	210	220	230	
	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCCG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTCCGCG
 151 CCGAACGCCG CCGCCGCCG CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGLGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAEVK HPVSQGM IQM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggaaca tccaccctgc tgaatatgat tgcgggcatc
151 gtcggcgccg acggcggcga aattcggtcg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctcgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacgggtg gcaactggcg gcgcttttgt tgcgcgcctc
451 tccctgctgt tgctggatga atcgttttcc agtttgaca cgcatttgcg
501 cgaccggctg cgccgtatga ccgcgaacg catccgcaag gccggcatcc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac gccggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtgca ggctgcgccg ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaatgca cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801 ctgctccggg ctttccggcg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacgcta tttccgaaa cggtagcggtc
901 cgcattccgg tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTEAIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLRL LSAVHPEHGE LTLNLTVGQH TDGISNGTGV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1   ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GGCGGTTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGAGAGAA ACATTACCCG

```

```

201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGGC CTGGAAAATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTTGGACGA ATCGTTTTTC AGTTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCCG CTGATGGGTT
701 TGCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLELNLCKR FGNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
  51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
 101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
 151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
 201 EIAVMHKGRI LQYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
 251 DQDGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMRHA GAVSGKDTVR
 301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

```

              10      20      30      40      50      60
m593.pep      MLELNLCKRFGNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGEIWL
              |||||  ||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGEIRL
              10      20      30      40      50      60

              70      80      90      100     110     120
m593.pep      NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEAEERLAMAALAEVG
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG
              70      80      90      100     110     120

              130     140     150     160     170     180
m593.pep      LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK
              130     140     150     160     170     180

              190     200     210     220     230     240
m593.pep      GGIPAVLVTHSPEEACTTADEI AVMHKGRI LQYGPETLVKTPSCVQVARLMGLPNTDDN
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           GGIPAVLVTHSPEEACTTADEI AVMHEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD
              190     200     210     220     230     240

```

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	::: :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGA CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGGGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TCGGGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCA CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACC GAGCCTGAN AAACTTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GCGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCCGAAG AGGCCTGCAC GCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGTTT CAAACGCCTG CCGGCGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGGKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DQDGMCECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRDPDGGEIWL					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRDPDGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAEERLAMAALAEVG					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPXKLSGGGKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
a593	LENEHRKPXKLSGGGKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLPNTDDN					

g594.seq..

```
1 atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51 tctcgtttt agcatactcc ggctgctgtt ccgcaccgga attgggatcg
101 gtaagttcgc cgttcaggcc tttcagggtc ttaagctgct gatctgtacg
151 gttgagcacc caaatcggtt tgccttgcca ctggcggtc agcagctgac
201 ccgcttcgat ttactgaca tccacctcga cgcgagcacc ggagccttg
251 gctttttccg aagggaaaaa actggccaca aacggcggtg ccaccccaa
301 tgctgccact ccgccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttgtt gattttctta ttattccatta ttcagtcgtc ctaatatatt
401 gggaatgcgc agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tattttaaatt aaggtaa
```

g594.pep

1	MGADTDGDKD	VRLNRT	<u>GLVF</u>	SILRL	LFRIG	IGIGKFAVQA	FQVFKLLICT
51	VEHPNREFALP	LGGQQLTRED	FTDIHLDGST	GGLGFFRREK	TGHKRRCHTQ		
101	CCHSARAAGR	KCQETAAAVV	<u>DFLI</u>	<u>IHSYV</u>	<u>LIFW</u>	E CRAIK	HCNFTQFAVI
151	LKALFKIR*						

m594.seq	1	51	101	151	201	251	301	351	401	451
	ATGGGTGCAG	ATACCGATGG	CGACAAGGAT	GTTCCGGCTTA	ATCGAACGGG					
	TCTCGTTTTT	AGCATACTCC	GGCTGCTGTT	CCGCATCGGA	ATTGGGATCG					
	GTAAGTTCGC	CGTTCAGGCC	TTTCAGGTC	TTAAGCTGCT	GATCTGTACG					
	GTTGAGCACC	CAAAATCGTT	TGCCCTTGCCA	CTCGGCGGTC	AGCAGCTGAC					
	CCGCTTCGAT	TTTACTGACA	TCCACCTCGA	CGCAGCACC	GGCGGCTTGG					
	GCTTTTTCCG	AAGGGAAAAA	ACTGGCCACA	AACGGCGTTG	CCACACCCAA					
	TGCTGCCACT	CCGCCCGCGC	CGCAGGTCGC	GAGTGT CAGG	AAACGGCGGC					
	GGCCGTTGTT	GATTTCTTGA	TTATCCATTA	TTCAGTCGTC	CTAATATTTT					
	GGGAATACCG	AGCCATAAAA	CGTTGCAATT	TTACCCAGTT	TGCAGTGATA					
	CTCAAAGCAT	TATTTAAAT	AAGGTAA							

m594.pep

1	MGADTDGDKD	<u>VRLNRTGLVF</u>	<u>SILRLLF</u>	IGIGKFAVQA	FQVEKLLICT
51	VEHPNRFALP	LGGQQLTRFD	FTDIHLDGST	GGLGFFRREK	TGHKRRCHTQ
101	CCHSARAAGR	<u>ECQETAAAVV</u>	<u>DFLIHYSV</u>	<u>LIFWEYRAIK</u>	RCNFTQFAVI
151	LKALEKIR*				

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATAACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggggtt
51  gaccgcgtgc cagccgcccg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcgggt cggtcggtat cgccgtcaac

```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttggaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacgca accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacgg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcacccaaa
```

1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRIGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCACTAT CGCCGTCAAC
 151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGTGAAA AACTGTCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGTA CCGATGTGTA AGCCCTGCAA AAAGAAATCG ACGCATTTGC
 801 GTTCTCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGTG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCGG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CTTGCCCAA CTTGCGGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTN EGGSVSIQAVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRIGILGLK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALSVMALGLTACQPPEAEKAAPASGEAQTN EGGSVSIQAVNDNACEPMELT					
g595	MRKFNLALSVMALGLTACQPPEAEKAAPASGETQSAN EGGSVGIQAVNDNACEPMNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120

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m595.pep	VPSGQVVFN	IKNNSGRKLEWEIL	KGVMVVD	DERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFN	IKNNSGRKLEWEIL	KGVMVVD	DERENIAPGLSDKMNRLLPGEYEMTCGLLT
	70	80	90	100 110 120
m595.pep	130	140	150	160 170 180
	NPRGKLVVTD	SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE		
g595	NPRGKLVVAD	SGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE		
	130	140	150	160 170 180
m595.pep	190	200	210	220 230 240
	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGA	KDAGFTGFHRIEYALWVEK	
g595	KAKSLFAATR	VHYERIEPIAELFSELD	PVIDACEDDFKDGA	KDAGFTGFHRIEHALWVEK
	190	200	210	220 230 240
m595.pep	250	260	270	280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVG	GASELIEEVAGSKISGEED	DRYSHTD	
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVG	GASELIEEAAGSKISGEED	DRYSHTD	
	250	260	270	280 290 300
m595.pep	310	320	330	340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD	TNFKQVNEILAKYRTKDG	FETYDKLG	
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD	TNFKQVNEILAKYRTKDG	FETYDKLS	
	310	320	330	340 350 360
m595.pep	370	380	389	
	EADRKALQASINALAEDLAQLRGILGLKX			
g595	EADRKALQAPINALAEDLAQLRGILGLKX			
	370	380		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595.seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GGAAGTACG	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGAAA	AAGTGTCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGCGGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAAGTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCGTCCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGAATAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep

1	MRKENLTALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN
51	DNACEPMELT	VPSGQVVFN	KNNSGRKLEW	EILKGVMVVD	ERENIAPGLS

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

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m595/a595 99.7% identity in 388 aa overlap

```

              10      20      30      40      50      60
m595.pep      MRKFNLTA SVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI AVNDNACEPMELT
              |||||||
a595           MRKFNLTA SVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI AVNDNACEPMELT
              10      20      30      40      50      60

              70      80      90     100     110     120
m595.pep      VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
              |||||||
a595           VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
              70      80      90     100     110     120

              130     140     150     160     170     180
m595.pep      NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
              |||||||
a595           NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
              130     140     150     160     170     180

              190     200     210     220     230     240
m595.pep      KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
              |||||||
a595           KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
              190     200     210     220     230     240

              250     260     270     280     290     300
m595.pep      DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
              |||||||
a595           DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
              250     260     270     280     290     300

              310     320     330     340     350     360
m595.pep      LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG
              |||||||
a595           LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG
              310     320     330     340     350     360

              370     380     389
m595.pep      EADRKALQASINALAEDLAQLRGILGLKX
              |||||||
a595           EADRKALQASINALAEDLAQLRGILGLKX
              370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1   ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgacagaccg ctacttctc gacaacgccg ccgaatggat tttggaactc
151 gaccgcgga cggcattcc gtggaaaggc aattactcgt cttggtcgga
201 gcagaaagaa aaacgcttgg aaaacgaggg gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcgttt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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451   ttcggcgata aagtgcctgat tgacggtttg agcttcaaag tgccggcgagg
501   cgcgattgtc ggcacatcatc gcccgaacgg cgcggggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaatc
601   gggcaaacgg tgaaaatgag cttgattgac caaagccgag aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccggc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcgggcgt ctgcacttgg caaaaacctt gttggggcgg ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgag
901   ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcaccaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLENEAKSE AARVKAMKQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYEY QKRNETQEIF IPVAERLGNE VIEFVNVSXS
151 FGDKVLIDGL SFKVPAGAIIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSDQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTCTTTT TTCCCCGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGCC
451 GCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CCGCGGTGAA AAACGCGCGG TTGCTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAA GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGCCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTA AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGCAGGTT GTTCAGTTTG AAATTCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 TCGCAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCCCTG
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCTT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTCTTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

```

1  MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AOKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPS GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGLHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

```

m596  g596      98.4% identity in 373 aa overlap

      160      170      180      190      200      210
m596.pep  LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDPEPTNHLDAESVEWLEQFLVRFPGTV
g596      |||||
      MLLLDPEPTNHLDAESVEWLEQFLVRFPGTV
                        10      20      30

      220      230      240      250      260      270
m596.pep  VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
g596      |||||
      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
              40      50      60      70      80      90

      280      290      300      310      320      330
m596.pep  LEWVRQNAKGRQAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
g596      |||||
      LEWVRQNAKGRQAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
              100      110      120      130      140      150

      340      350      360      370      380      390
m596.pep  FGDKVLIDDLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPSGEVKIGQTVKMSLID
g596      |||||
      FGDKVLIDGLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPSGEVKIGQTVKMSLID
              160      170      180      190      200      210

      400      410      420      430      440      450
m596.pep  QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
g596      |||||
      QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
              220      230      240      250      260      270

```

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	EPSNDLDVETLRALED	DALLEFAGSVMVISH	DRWFLDRIATHIL		
	:					
g596	LHLAKTLLGGGNVLLLD	EPSNDLDVETLRALED	DALLEFAGSVMVISH	DRWFLDRIATHIL		
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGN	YQEYADKKRRLG	EEGAKPKRIKYK	PVTRX	
g596	ACEGDSKWVFFDGN	YQEYADKKRRLG	EKGAKPKRIKYK	PVTRX	
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTTCTTTC TTCCCCGGCG
101 CGAAAAATCGG TTTGCTCGGT TTGAACGGCG CGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTTGCGG AACACGAATT GGAATCGCT
451 GCCGACGCGC TGCCTTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TCGGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGGAACG GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCCG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGACGACC GCTGGTTCTT CGACCGTATT GCTACGCATA TCTTAGCCTT
1551 CGAAGGCGAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1   MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLFSKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDS GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN YQEYADKKRR LGEEGTPKPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFP GTVVAVTHDRYFLDNAAEWILEDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFP GTVVAVTHDRYFLDNAAEWILEDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNIEVFNVS KSF GDKVLIDDL SFKVPAGAI VGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEVFNVS KSF GDKVLIDDL SFKVPAGAI VGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTL FKMISGKEQ PDSGEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTL FKMISGKEQ PDSGEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR LHLAKTLLSGGNVLLLD E P S N D L D V					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGR LHLAKTLLSGGNVLLLD E P S N D L D V					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGN YQEY EADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGN YQEY EADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGAAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGCGGAA CAGACGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TTcaggAtgc ggAagcaaaa agaAAATTGG CTGAagcCaa
651 actGgcgga gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCGGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggc GATGTTTGA AAGCGGTGTT CTATTCCACT
901 GCGCCTGCAA CGGTTGAAAG CATTGCGCcg gAACggttaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCACG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTGCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK QREAWDKFOK
51 LNTELNRKLT EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QKALAVOEQ KINNELARLK KIQANVQSL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQV VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAAACAGC CGAGGCTTGG GACAAAGTCC AAAAACTCAA TACCGAGCTG
151 AACCCTTTGA AAACGGAAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCTGTGTCC
251 TGAAGAACCG CGAACC GGCT CAGAAAAACC GCTTTTTCG TATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGG AAAAAACGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAAT CAACAATGAG CTGCCCCGTT
401 TGAAGAAAAA TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAAGCCGC AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAACTGC TGGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCCGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCATAT TTGGAAGGCG GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAGATG GTCGTGGTGC ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV KDLKQKQKAL AVQEQKINNE LARLKKIQAN VQSLLKQGV
151 TDAEQTESR RQNAKIAKDA RKLLEQKQNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKRLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDNRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDTGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGVLNPS SWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

```

      10      20      30      40      50      60
g597.pep  MLLHVSNSLKLQEEIRIRQERIRQERIRQARGNLSVNRKQREAWDKFQKLNTELNLRLKT
m597      MLLHVSNSLKLQEEIRIRQ-----ARGNLSVNRKQREAWDKFQKLNTELNLRLKT
      10      20      30      40      50

      70      80      90     100     110     120
g597.pep  EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
      60      70      80      90     100     110

      130     140     150     160     170     180
g597.pep  QOKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE
m597      QOKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
      120     130     140     150     160     170

      190     200     210     220     230     240
g597.pep  QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM
m597      QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
      180     190     200     210     220     230

      250     260     270     280     290     300
g597.pep  SNLTAEDRNIQAPSVMGIGSADGFSRMQGRKKPVDGVPTGLFGQNRSGGDVWKGVFYST
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGRKKPVDGVPTGLFGQNRSGGDIWKGVFYST
      240     250     260     270     280     290

      310     320     330     340     350     360
g597.pep  APATVESIAPGTVSYADELDGYGKVVDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT
m597      APATVESIAPGTVSYADELDGYGKVVDHGENYISIIYAGLSEISVKGGMVAAGSKIGS
      300     310     320     330     340     350

      370     380     390
g597.pep  SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX
m597      SGSLPDGEEGLYLQIRYQGQVLNPSGWIRX
      360     370     380

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

```

a597.seq
1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTC CGTTTCGTAT CGGGGAAC TA AAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCCGTGAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAAG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGCGGAA CAGACGGAAG CCGCAGACA
501 GAATGCCAAA ATCGCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCAGCAGC TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGCGGCG GATGTTTGGA AAGGCGTGTT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA

```



```
951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```
1 MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNR LKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ OKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLNPSWIR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

```
          10      20      30      40      50      60
a597.pep  MLLHVSNSLKQLQEERIRQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNR LKT
m597      MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNR LKT
          10      20      30      40      50

          70      80      90     100     110     120
a597.pep  EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90     100     110

          130     140     150     160     170     180
a597.pep  QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
m597      QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

          190     200     210     220     230     240
a597.pep  QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
m597      QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          180     190     200     210     220     230

          250     260     270     280     290     300
a597.pep  SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDVWKGVFYST
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

          310     320     330     340     350     360
a597.pep  APATVESIAPGTVSYADELDGYGKVVVDHGENYISYIYAGLSEISVGKGYMVAAGSKIGS
m597      APATVESIAPGTVSYADELDGYGKVVVDHGENYISYIYAGLSEISVGKGYMVAAGSKIGS
          300     310     320     330     340     350

          370     380     390
a597.pep  SGSLPDGEEGLYLQIRYQGQVLNPSWIRX
m597      SGSLPDGEEGLYLQIRYQGQVLNPSWIRX
          360     370     380
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

g601.seq

```

1  ATGTTCCCAA CCGGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCTATGAT GGGCATCGCC TCGGTGCGCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CCGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcgggtca
551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

g601.pep

```

1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTAA KAVMSRSARV IMESWVRVPD
201 DCF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

m601.seq

```

1  ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCGTATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACAGGTG
601 CCTGAGGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

m601.pep

```

1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDQGWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

      |||||:|||||
g601  TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLPVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSTGLRVGAAAECDGQWT
      |||||:|||||
g601  KLHHAMMGIA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHGHPSTGLRVGAAAECDGQWT
      130     140     150     160     170

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |:|||||:|:|:|:|:|
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
 51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101  ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151  AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201  GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251  ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCTCC
301  AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351  GAGCATGGGC AAATTCGACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401  TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451  GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501  CGTCGGTGCA GCCCGCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551  CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTCAGGGTG
601  CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101  SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151  GGTRKEVRFG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201  PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.pep MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      |||||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.pep KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
      |||||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSTGLRVGAAAECDGQWT
      |||||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSTGLRVGAAAECDGQWT
      130     140     150     160     170     180

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
 51 CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTTGC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
  1 MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
 51 LIDRQIAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLsAA
101 CLQMRDYITC FWRlh*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCCTTCTGCT
 51 CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
  1 MLLHQCDKTR HMRPILLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
 51 LIDRQIAQIS AGLHVCNSVH ELFFLNIHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPILLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNIHVIEMCAWYGVSAGEYTVN---LQMRDYITRFQQLHX					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLsAACLQMRDYITCFWRlhX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
 51 CGGCGAGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
  1 MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
 51 LIDRQIAQIS AGLHVCNSVH ELFFLNIHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNCLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITREFXQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITREFXQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AAATAACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TCGTCAGTT CATCGCTCAA
201 AGGCGCGCTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGGAACGCCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCACGGCG GCGAAAAATA TCACGAGTCC
451 GTCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCCTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGAATGGG TACACGTTGC GCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCGAAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGCTACGGCA ATTCGGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCCG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGND A RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPOTTRRNI
51  MSDQLILVLN CVSSSLKGA V IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPNANISIL AAQEHFPGLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTL EIAAD EGREGARLAL
351 EVMTCLRAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYNGSGIISP TDSSPAVLVV PTNEELMIAC DTAEAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCTGAT GTCTGC.CTT
101 TTTTACAGCA CCCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

1	LSSRRRGRNN	DRKCGIRFAQ	RGLRLKHLAPD	VCFXFSDDPTL	KKQPQTTRRN
51	IMSDQILILVL	NCGSSSLKGA	VIDRXSGSVV	LSCLGRLTT	PEAVITFNKD
101	GNKRQVPLSG	RNCHAGAVGM	LLNELEKHGL	HDRIKAIGHR	IAHGGEKYSE
151	SVLIDQAVMD	ELNACIPLAP	LHNPANISGI	LAAQEHFPGL	PNVGVMDTSF
201	HQTMPERAYT	YAVPRELRKK	YAFRRYGFHG	TSMRIYAPEA	ARILGKPLED
251	IRMIIAHLGN	GASITAIKNG	KSDVTSMGFT	PIEGLVMGTR	CGDIDPGVYS
301	YLTSHAGMDV	AQVDEMLNKK	SGLLGISELS	NDCRTLEIAA	DEGHEGARLA
351	LEVMTYRLAK	YIASMAVCGC	GVDALVFTGG	IGENSRNIRA	KTVSYLDLFLG
401	LHIDTKANME	KRYGNSGIIS	PTDSSPAVLV	VPTNEELMIA	CDTAELAGIL
451	*				

Homology with a predicted ORF from *N.gonorrhoeae*

m603/g603

BNSDOCID: <WO__9957280A2_1_>

957

```

g603      LAAQEHFPGLPNVGVMDSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
           180      190      200      210      220      230

           250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
           |||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
           240      250      260      270      280      290

           310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALAEVMTYRLAK
           |||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISELPND CRTLEIAADEGREGARLALAEVMTCLRAK
           300      310      320      330      340      350

           370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
           |||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
           360      370      380      390      400      410

           430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
           |||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
           420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGTCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTGAGACGA CCCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAACGTC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCAGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCGC TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCC CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGTTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGGCGGT ATCGCGGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT CCGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRCLKHTPPN AHPFSDDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSLGLERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHN PANISGI LAAQEHFPGL PNVGVMDSF

```

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGENSRNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

m603.pep	10	20	30	40	50	60
	LSSRRRGRNNDKRCGIRFAQGRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL					
a603	10	20	30	40	50	60
	LSSRRRGRNNDKRCGIRFAQGRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL					
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNGKQVPLSGRNCHAGAVGM					
a603	70	80	90	100	110	120
	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDGNGKQVPLSGRNCHAGAVGM					
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHHGGEKYSVSLIDQAVMDELNACIPLAPLHNPANISGI					
a603	130	140	150	160	170	180
	LLNELEKHGLHDRIQAVGHRIAHHGGEKYSVSLIDQAVMDELNACIPLAPLHNPANISGI					
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA					
a603	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA					
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	250	260	270	280	290	300
	ACILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
a603	310	320	330	340	350	360
	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS					
a603	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS					
m603.pep	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELAGILX					
a603	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELVGILX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GGCGGGTTTC GGCGTGC GCGCGGCGGC GGCTTCGGAT

g604 . pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
51  VGGVYGFAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101 KFFQGGIIV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI*

```

m604.seq

1	ATGCCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCTGCG	GCAAGGTTGA
51	CCAGCGTACC	GGGTACGGCG	GCGGCGGTCG	CAATGGCAAC	AGAGGCGGTA
101	CCCATCATCG	CGTGGTGCAG	TTTGCCCATG	CTCAGGGCGC	GTACCAGCAA
151	ATCGATGTCTG	GCGGCGTTCA	CGGTTTTGCC	ACTGGAGGCG	GTGTAATCGG
201	CGCAGCGCGC	GACGAAGGCG	ACTTTCCGGC	TGTGCGCGCG	AGCGGCAGCT
251	TCGGATACGT	CGCTGATCAG	ACCCATTTC	AGCGCACCGT	AAGCGCGGAT
301	TTTCTCGAAT	TTTTCCAAAG	CCGCGGCATC	GTTGTTGATG	TCGTCTTGCA
351	ACTCTTTGCC	TGTGTAGCCC	AAGTCGGCGG	CATTCAAGAA	AACGGTCGGA
401	ATGCCCCGCT	TGATGAGCGT	GGCTTTCAAA	CGGCCTATAT	TCGGCACATC
451	AATTTTCATCG	ACCAAATTGC	CGGTTGGGAA	CATACTGCCT	TCGCCGTCGG
501	CTGGATC				

m604 . pep

```

1  MPEAHFFTRS AACGKVDQRT GYGGGGGRNGN RGGTHHRVVO FAHAQGAYQQ
51  IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGVADQ THFQRTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604 / g604

```

      10          20          30          40          50          60
m604.pep MPEAHFFTRSAACGKVDQRTGYGGGGGRNGNRGGTHHRVVFQFAHAQGAYQQIDVGGVHGFA
           ||||||| :|| |:|| :|| ||||| :||| :||| :|||
g604      MPEAHFFTRSAACGKVDQRTEHGGG--DGDRGDAHHSVVQFQFAHAQGAIRQIDVGGVYGFA
           10          20          30          40          50

      70          80          90          100         110         120
m604.pep TGGGVIGGGRDEGDFFRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
           :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g604      AGGGVIGGGRDEGGFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGGIVVDVVLQLFA
           60          70          80          90          100         110

      130         140         150         160         169
m604.pep CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
           ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g604      RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX
           120        130        140        150        160

```

a604.seq

1	ATGCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCTGCG	GCAAGGTTGA
51	CCAGCGTACC	GGGCACGGCG	GC GGCGGTTCG	CAATGGCAAC	AGAGGCGGTA
101	CCCATCATCG	CGTGGTGCAA	TTTGCCCATG	CTCAGGCGCG	GTACCAGCAA
151	ATCGATGTCG	GCGGCATTCA	CGGTTTGGCC	ACTGGAGGCG	GTGTAATCGG

```
201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTTCAGGAA AACGGTCGGA
401 ATGCCCCGCT TGATGAGCGT GGCTTTCAA CCGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTCG CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```
a604.pep
  1 MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
 51 IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVGVWIK KFDLYFGCRE RYAVELKIAC FQNCVAVLHRY
201 MGNNGFADV FLPDFCADAV *
```

m604/a604 97.0% identity in 169 aa overlap

```
          10      20      30      40      50      60
m604.pep MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
          |||||:|||||:|||||:|||||:|||||:|||||
a604      MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA
          10      20      30      40      50      60

          70      80      90     100     110     120
m604.pep TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA
          |||||:|||||:|||||:|||||:|||||:|||||
a604      TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVVDVVLQLFA
          70      80      90     100     110     120

          130     140     150     160     169
m604.pep CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK
          |||||:|||||:|||||:|||||:|||||
a604      RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE
          130     140     150     160     170     180

a604      RYAVELKIACFQNCVAVLHRYMGNNGFADVFLPDFCADAVX
          190     200     210     220
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```
g605.seq
  1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGA
 51 AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgcccgcga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCcgCAAC GCAGGCAAAT CCGCGGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCCACA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT
```

```

951 CAACGACGAC CGCTTTGCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGGATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCGG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MITEMQORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFED HRIDLFDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGOEKVN KIYDPACGSG SLLLOAKKQF DEHIIIEGFF
251 GQINHTTYN LARMNMFHVN VYNKPHIEL GDTLTNPCLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG
351 RAAIVSFPFI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVLKSHKNDT DIQFIDASGF FKKETMNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCGGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCCGCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCCT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCC CCGCAGGCGT ACTTGCCCGG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGGATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MITEMQORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEIHNHTTYN LARMNMFLHN VNYNQFHIEL GDTLTNPKLK DSKPFDIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

m605.pep	MMTEMQRAQLHRQIWKIADEV	RGAVD	GWDFKQYVLGTLFYRFISENFTDYM	QAGDSSID
g605	MMTEMQRAQLHRQIWKIADEV	RGAVD	GWDFKQYVLGTLFYRFISENFTDYM	QAGDSSID
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS			
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS			
m605.pep	GYPSEQDIKGLFDDFDTTSSRLG	STVADKNKRLAAVLKGV	AELDFGNFENHHIDLFGDAY	
g605	GYPSEQGIKGLFDDFDTTSSRLG	STVADKNKRLAAVLKGV	AELDFGNFEDHRIDLFGDAY	
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLOAKKQF			
g605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLOAKKQF			
m605.pep	DEHIEEGFFGQEIHNHTTYNLARMNMFLHN	VNYNQFHIELGDTLTNPKLK	DSKPFDIVS	
g605	DEHIEEGFFGQEIHNHTTYNLARMNMFLHN	VNYNKFHIELGDTLTNPKLK	DSKPFDIVS	
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI			
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI			
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF			
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF			
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVP	PHIAQNAAQQT	VKDNGYNLAVSSYVEAEDTRE	
g605	FKKETNNNVLTEEHIAEIVKLFADKADVP	PHIAQNAAQQT	VKDNGYNLAVSSYVEAEDTRE	

430 440 450 460 470 480

490 500 510

a605.seq

1	ATGATGACCG	AAATACAACA	ACGCGCCCAA	CTGCACCGCC	AAATTTGGAA
51	AATTGCCGAC	GAAGTACGCG	GCGCGGTGGA	TGGCTGGGAC	TTCAAACAAT
101	ACGTTCTCGG	CACACTTTTC	TACCGCTTTA	TCAGCGAAAA	CTTTACCGCA
151	TATATGCAAG	CAGGCGACAG	CAGTATTGAT	TACGCCGGTA	TGCCGGACAG
201	CATCATCACG	CCCGAAATCA	AAGACGATGC	CGTCAAAGTC	AAAGGCTATT
251	TCATCTACCC	CGGCCAGCTT	TTTTGCAATA	TTGCCGCCGA	AGCCCATCAA
301	AACGAAGAGC	TCAACACCAA	GCTGAAAGAA	ATTTTTACCG	CGATTGAAAG
351	CTCCGCCCTC	GGCTATCCGT	CCGAAACAAG	CATTAAGAAGC	CTGTTTGACG
401	ACCTTCGACAC	CACCAGCAGC	CGGCTCGGCA	GACCCGTTGC	GCACAAGAAC
451	AAACGCCTTG	CCGCCGTCTT	AAAAGGCGTG	GCGGAACTCG	ATTTCCGGCAG
501	TTTTGAAGAC	CACCACATCG	ACCTTTTCGG	CGATGCCTAC	GAATACCTGA
551	TTTCCAAATA	CGCTGCCAAC	GCAGGCCAAT	CCGGCGGGCA	ATTTTTTACC
601	CCGCAAAGCG	TATCCAAGCT	GATTGCGCGG	CTGGCGGTGC	ACGGGCAGGA
651	GAAAGTAAAC	AAAATCTACG	ATCCAGCTTG	CGGCTCGGGC	AGCCTGCTCT
701	TGCAGGCGAA	AAAACAGTTT	GACGAGCACA	TCATCGAAGA	AGGCTTCTTC
751	GGGCAGGAAA	TCAACCACAC	CACCTACAAC	CTCGCCCGCA	TGAATATGTT
801	TCTGCACAAC	GTCAATTACA	ACAATTTCCA	CATCGAATTG	GGCGACACAC
851	TGACCAATCC	CAAACTCAAA	GACAGCAAAC	CTTTTGATGC	CGTCGTTTTC
901	AATCCGCCCT	ATTCCATCAA	CTGGATAGGC	AGCGGCGACC	CCACCTTAAT
951	CAACGACGAC	CGCTTTTGCC	CTCGAGGCGT	ACTCGCCCCG	AAATCCAAAG
1001	CCGATTTTGC	CTTCATTCTG	CACGCACTGA	ACTACCTTTC	CGGCAGAGGC
1051	CGCGCCGCCA	TCGTCTCATT	CCCCGGCATT	TTCTATCGCG	CGGCGCGAGA
1101	GCAGAAAATC	CGCCAATATC	TGGTGGAGGG	CAACTACGTG	GAAACCGTCA
1151	TCGCCCTTGC	GCCCAATCTC	TTTTACGGCA	CCGGCATCGC	CGTCAATATA
1201	CTGGTTTGTG	CCAAACACAA	AGACAATACC	GACATCCAAT	TCATCGAGCC
1251	AGGCGGCTTC	TTTAAAAAAG	AAACCAACA	CAACGCTCTA	ACCGAAGAAC
1301	ACATTGCCGA	AATCGTCAAA	CTCTTCGCCG	ATAAAGCCGA	TGTGCCGCAT
1351	ATCGCCCAAA	ACGCCGCCCA	GCAAACCGTC	AAAGACAACG	GCTACAACCT
1401	CGCCGTGAGC	AGCTATGTGT	AACCCGAAGA	CACCCGCGAA	ATTATCGACA
1451	TCAACACAGT	TAACGCCGAA	ATCAGCGAAA	CCGTTGCCAA	AATCGAACGG
1501	CTCGCGCGTG	AAATTGACGA	AGTGATTGCA	GAGATTGAAG	CATGA

a605.pep

1	MMTEIQQRAQ	LHRQIWKIAD	EVGRAVDGWD	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGYFIYPGQL	FCNIAAEAHQ
101	NEELNTKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	AELDFGSEFD	HHIDLFPAGD	EYLSINYYAN	AGKSGGEFFT
201	PQSVSKLIAR	LAVHGQEKVN	KIYDPACGSJ	SLLLQAKKQF	DEHIIIEEGF
251	GQEIHNHTYTN	LARMNMFLLN	VNYNKFHIEL	GDTLTNPKLK	DSKPFDAVVS
301	NPPYSINWIG	SGDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYSLSRG
351	RAAIVSFFGI	FYRGGAEQKI	RQYLVEGNYV	ETVIALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTV	KDNGYNLAVS	SYVEPEDTRE	IIDIQQLNAE	ISETVAKIER
501	LRREIDEIVA	EIEA*			

	10	20	30	40	50	60
m605.pep	MMTEMQQR RAQL HRQIW KIA DEV RGAV DGWD FKQY VLG TLFY RFISE NFTD YMQAGDSSID					
	:					
a605	MMTEIQQR RAQL HRQIW KIA DEV RGAV DGWD FKQY VLG TLFY RFISE NFTD YMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFTYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSA					

```

a605      |||||
YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS
          70      80      90      100     110     120

m605.pep      130      140      150      160      170      180
GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEELDFGNFENHHIDLFGBAY
a605      |||||
GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEELDFGSFEDHHIDLFGBAY
          130      140      150      160      170      180

m605.pep      190      200      210      220      230      240
EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF
a605      |||||
EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF
          190      200      210      220      230      240

m605.pep      250      260      270      280      290      300
DEHIIIEGFFGQEIHNHTTYNLARMNMFHNVNYNQFHIELGDTLTNPCLKDSKPFDAIVS
a605      |||||
DEHIIIEGFFGQEIHNHTTYNLARMNMFHNVNYNKFHIELGDTLTNPCLKDSKPFDAVVS
          250      260      270      280      290      300

m605.pep      310      320      330      340      350      360
NPPYSINWIGSDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGAAIVSFPGI
a605      |||||
NPPYSINWIGSDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGAAIVSFPGI
          310      320      330      340      350      360

m605.pep      370      380      390      400      410      420
FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGI AVNVLVLSKHKDNTDIQFIDASGF
a605      |||||
FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGI AVNVLVLSKHKDNTDIQFIDAGGF
          370      380      390      400      410      420

m605.pep      430      440      450      460      470      480
FKKETNNNVLIEEHIAEIVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEAEDTRE
a605      |||||
FKKETNNNVLTEEHIAEIVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEPEDTRE
          430      440      450      460      470      480

m605.pep      490      500      510
IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
a605      |||||
IIDIKQLNAEISETVAKIERLRREIDEVIAEIEAX
          490      500      510

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGTGCGGAAG TCATCGACAC
51  GCCGcgCACC GAAGAAGAAG CCTGGCTTCT GAACACTGTC GAAGCCCAAg
101 cgcGGCAATG GAATCTGAAA ACGCCAGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCacc ggtttgctcg accaTatgaC GCGCGACgaa gtggaagccg
251 tgTTGGCGCA CGAAATGGCG CACGTCGGCA ACGGCGACAT GGTTCAGCTG
301 ACGCTGAtTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT AGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCCTGATTG TCATGTGGTT CAGCCGCCAA CGCGAATACC GCGCCGAcgc
501 gggCGcggCA AACTGGTTCG GCGCACCgAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTCG GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTCGCTGGA
651 CAACCGTATC GCGCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLK TPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLK TPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRRIAN					
g606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRRIAN					
	70	80	90	100	110	120
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTGGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTCAGCATG GTATTCCAAA TCCTGTTCCG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AACTGGTCG GCGCGCGGAA AATGATTTC GGCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VFVLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPEPNAFATGAS					
a606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

g607.seq

```

1  ATGCTGCTCG accTcgaCCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCGATGATT TGATGTGGGC
351 GCGGATTACG CCGTCCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

```



```

601 GGTTCGCGCG TGGCGACAAT GCGCGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGAAGTACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAgccaGcg cGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTtccgCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATCCGTTT CCGCGTGGCA
1051 AGCATGTACA ACGATGATCC GGCAGTTTTA AGCATCGCCT CCACCGTCTT
1101 GCTGTTCCGC GGCCTGTtcc aACCGGCAGA CTTACCCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGILIGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQVVGISLS GILYMIPQSV
301 GSACTVIRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFMIH
401 AAAPWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTGTG GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAAGTG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGTGTTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGCGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGAAGTACAG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAATC
751 GCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGCGCA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATCCGTTT CCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTATA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGC GCGTGTTC AACCAGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSSF PVFLKEVRLL TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

101 IWFGFLGVPF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRLHAYT SSLNRPRILIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQVVGISLS GILYMIQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFERSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAFAWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	: : : : :					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVPFGMVLMWAAIT					
	: : : : :					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGLLIGIFGMILMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLHAYTSSLNRPRILIMLVSFAAFVLN					
	: : : : :					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLHAYASSLNRPRILIMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVF WFSALALWIYIAKENFFRPFGLTAKFGKPD					
	: : : : :					
g607	VPLNYIFVYGKFGMPALGGAGCVATMAVF WFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQVVGISLSGILYMIQSV					
	: : : : :					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQVVGISLSGILYMIQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRRARYISGVSLVLGWMLAVITVLSLVLFERSPLVSMYNNDDPAVL					
	: : : : :					
g607	GSAGTVRIGFSLGRREFSRRARYISGVSLVSGWVLAVITVLSLVLFERSPLASMYNNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
	: : : : :					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
	: : :					
g607	MGIYGFWTALIASLTIAAIALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTTC GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCCA ACTGGGTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTCACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTIONG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTTCGTT
801 TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTCC AACCAGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLL TALALEMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRAHAYT SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMPIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNNPVLV SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMTFH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFVSFLKEVRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFVGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFVGMVLMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYASSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240
              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
              250      260      270      280      290      300
              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVLGWM LAVITVLSLVLFERSPLVSMYNNDAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWM LAVITVLSLVLFERSPLVSMYNNDAVL
              310      320      330      340      350      360
              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVP MFIHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVP MFIHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420
              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCatCaaa CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LOGGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
g608	MSALLPIINRLILQSPDSRSELT SFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGDLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGKIQIGRNIAEQIGGFSRESSESANIGNEALADCLDEISRLRDGVERLNERLDR					
g608	RATDIGHGKIQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCT TGCCGACTGC CTCGACGAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```

m608.pep    MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLGRITEDGLLSAGNGFADTEI
a608        MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLGRITEDGLLSAGNGFADTEI
              10      20      30      40      50      60
              70      80      90     100     110     120
m608.pep    TFRNSAVQKILQGGEPEGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608        TFRNSAVQKILQGGEPEGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
              70      80      90     100     110     120
              130     140     150     160     170     180
m608.pep    RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRRLRDGVERLNERLDR
a608        RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRRLRDGVERLNERLDR
              130     140     150     160     170     180
              189
m608.pep    LERDIWIDX
a608        LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TGCCTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GGCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGGCCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTAGT TGGCCGTATG
351 CCCCCTCTTT CATTTACCCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRFHIDNF LDTDFGIGSQ ADGNVRTLIM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TGCCTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GGCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTAGT TGGCCGTATG
351 CCCCCTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

              10      20      30      40      50      60
m609.pep    MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60
g609        MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60
              70      80      90     100     110     120
m609.pep    RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGT RAKRGYGNHDLHTVAVCPVF
              70      80      90     100     110     120

```

```

g609      RLRFHIIIDNFLDITDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF
           70          80          90          100          110          120

           130
m609.pep  DFARETDIIIIQX
           |:|:|:|:|:|:|
g609      HFTREADIIIIQX
           130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```
a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAATCATCTTGA
51  TGCGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCCTGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCAATCTG TGGCCGATG
351 CACCGTCTTT CATTCGCCCG GTGAGGCTGA CATCATAATC CAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

```
a609.pap
  1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GFFGNVFFIG
 51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101  RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*
```

m609/a609 96.9% identity in 131 aa overlap

		10	20	30	40	50	60
m609.pep		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGVFFGNVFFIGAFEQAVELAA					
a609		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGVFFGNVFFIGAFEQAVELAA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHIIDDFLDTFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF					
a609		RLRLHIIDDFLDTFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF					
		70	80	90	100	110	120
		130					
m609.pep		DFARETDIIIQX					
		:					
a609		HFAREADIIIQX					
		130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1937>:

```
g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCTTAC  CGCAATGTTT  CGGCTTCGCG
51  TATGCGCCCT  ATGCGCAGGG  ATGATTTTTC  ACGCCGCGTG  ATGCGCGAGC
101  ATATGCTGAC  CGCCGATGAT  TTGATTATC  CGGTGTTCTG  ATTGGAGGGG
151  GCGGCGCGCG  AGGAGGATGT  GCCTTCTATG  CCGGCGGTGA  AGCGTCAGAG
201  TTTGGACAGG  CTGCTGTTTA  CGGCGGAAG  GCGGGTGAA  CTGGTATTTC
251  CGATGTTGGC  ACTCTTTCCC  TGGGTACGG  AAACAAAAAC  CGGGCGTCGG
301  CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  tccgagccTT
351  GCGCGAGAGG  TttccGgaac  tggggattat  gcaggtatgt  gcgctcGAtc
401  cttatacggt  gcacGGTCAG  GACGACTGA  CGGACgaaaa  cggttacGTG
451  ATGAatgATg  aaaCCGTAGA  AGTCTTGGTG  AAACAGGCTT  TGTCTATGTC
501  AGAGCGGGGC  ACGCAGGTCG  TTGCTCCTTC  CGATATGATG  GACGGGCGTA
551  TCGGCGCCAT  CCGCGAGGCT  TTGGAGGAT  CCGGACATAT  CCATACGCGG
601  ATTATGGCAT  ATTCGCGCAA  ATATGCTTCT  GCATTCTACG  GCGCCTTCCG
651  TGATGCGGTA  GGCAGTTCCG  GCAATTGGG  AAAGGCAGAT  AAAAAGACCT
701  ATCAGATGGA  TCTTGCAATT  ACCGATGAGG  CGCTGCATGA  GTTGGCGCCT
751  GATATTcAGG  AAGGTGCGGA  TATGGTGATG  GTAAGGCCGG  ATTGGCGGTA
```

```
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

```
g610.pep
1  MIGGLMQFFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  AAREEDVPSM PGVKRQSLDR LLFTAEAEVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGO DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAVAN
301 GWLDGGKVVL ESSLAFKRAG ADGILTYAI EAAKMLKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

```
m610.seq
1  ATGATTGGAG GGCTTATGCA GTTCTCTTAC CGCAATGTTC CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAG CTGCGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CCGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGCG GCGCAGGTGG TTGCCCCTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACCGATGT TGCAGGCAGC GATTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

```
m610.pep
1  MIGGLMQFFPY RNPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEAEVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGO DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AOVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAIAN
301 GWLDGGKVVL ESSLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
m610.pep	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGOGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM					
g610	FPELGIMTDVALDPYTVHGOGLTDENGYVMNDETVEVLVKQALCHAEAGTQVAPSDMM					
	130	140	150	160	170	180
m610.pep	DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					
g610	DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					


```

g610      DGRIGAIAREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTIYAYQVSGEYAMLQAAIAN
           |||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTIYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAAGDILTYAIEAAKMLKRK
           |||
g610      GWLDGGKVVLESLLAFKRAAGDILTYAIEAAKMLKRK
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGTATTTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGCT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGCGGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTGGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIARE LEDAGHIHTR
201 IMAYSAYAS AFYGPFRDAV GSSGNLGKAD KKTQYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVL ELLAFKRAAG ADGILTYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

```

```

m610.pep      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQVVAPSDMM
a610          FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQVVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
a610          DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
a610          TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
a610          GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCTGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctga
251 TcgcgGTCTa tggtttcCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gCTCAtgcCG TAGCGCGTTA
501 CCATTTTCGCG TGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMGKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIIVYGFP FHQGFARHFH
101 LVAVFIEDFV GNLLLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCTGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGCG TTTTCATCGA GGATTTGTa ggcaacCTGA TATTGCTCGT
351 CCAAAAATCCG GCGGATTTC CCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGCG AACGGgttac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTTCGCG CGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMGKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIIVDGFP FHQGFARHFH
101 LVAVFIEDFV GNLLLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

```

10      20      30      40      50      60

```

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFAHRLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GCTCATGCCG TAGCGCGTTA
501 CCATTTGCGC CGCCATTGGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFL
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFAHRLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFAHRLGCAFKVV
              130     140     150     160     170     180

```

m611.pep X

a611

X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq

```

1  ATGGGgcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51  AGCCTttgac tttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep

```

1  MGFGGNIARK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq

```

1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTTAA TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep

```

1  MGFGGNIARK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRRFFY GHSN*

```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIARKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINNTAVACLHIVGEVFADKAVE					
g612	MGFGGNIARKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
g612	KCAENVLFKVPPIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq

```

1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttT. AC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101 NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612 96.0% identity in 124 aa overlap

      10      20      30      40      50      60
m612.pep  MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612      MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
          10      20      30      40      50      60

      70      80      90     100     110     120
m612.pep  KCAENVLFKVPAlHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612      KCAENVLFEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
          70      80      90     100     110     120

m612.pep  GHSNX
          ||||
a612      GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTTCGT CGAggcagtc ggcaagggct tcgttgccgg
101 tgtttGcgGA CTCGGGTTCG CGGGAATC CGCCGATTG TTCGGCGATG
151 TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgtgcc
201 gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCCG
301 CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351 CCGTATCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
601 ATTTTACAGG CTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151 AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201 ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTTTCGGA CTCGGATTTC CGGGAATC CGCCGATTG TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
  
```

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLLPL
201  ILQA*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSAPAGSPPWRIFRIA					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1   ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTTCG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTCGCGGA CTCGGGTTTC CGGGAATATC TGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGCTCTGC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTGCGC CGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAACCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGACAGG TCAGGCGGTT GATGATGGGG AGGAGGCGCG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGACGCTT
601 ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1   MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSGS RENLPICSAM
51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFPN
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLTL
201 ILQA*

m613/a613    98.0% identity in 204 aa overlap

          10      20      30      40      50      60
m613.pep    MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP
a613         MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP
          10      20      30      40      50      60

          70      80      90     100     110     120
m613.pep    MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA
a613         MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA
          70      80      90     100     110     120

          130     140     150     160     170     180
m613.pep    LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKASSERLSGLCRIRRLMMG
a613         LLRKVISVSAKPFPAESKPSSVMRPASFPAMFRVSVLPAAKASSERLSGLCRIRRLMMG
          130     140     150     160     170     180

          190     200
m613.pep    RRADIFSDRGGECLLLLLPLILQAX
a613         RRADIFSDRGGECLLLLLTLILQAX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acggggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGATG ACAACCTGAT
201 TCAAACCCTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCGC GCTGACTGCC CTGTTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCgcta
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
601 GTGCCGTTCT TCAGCATTTC CGGTTCCGAT TTTGTGAAA TGTTCTGCGG
651 TGTCCGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGACA TCCGGGGCGG
951 CGAACAGatn ttGAACGTCC ATTCTaaaAAA AGTGCcttTG gacgaATCTg
1001 tggATTTATT GTCCCTCGCG CGCGGCACGC ccggtttTtTc cggcgcgat
1051 tTggcgaaac tggTcaacga agccccctg tttgccggcc gccgcaacaa
1101 agtgaaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFFTNA PLDDNLIQTL LKNKVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGUGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQX LNVHSKKVPL DESVDLLSLA RGTPTGFSAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACTTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
201 TAAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCGC GCTGGCTGCC CTGTTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAA CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCgcta
501 TCAAAGCCTG GCGGCGGCGG TGCCGCGCGG CATCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGAAA TGTTCTGCGG
651 TGTCCGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTTG ACCGCCAAGT GGTGTCCCC CTGCCGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGTTTTTTC CGCGCGGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:


```

m614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAAGEAG
201 VPFSSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVV PLDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVTPEEKPSALAAALFYSLLPVLLLIGAWFYFMRMQTGGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVTPEEKPSALTALFYSLLPVLLLIGAWFYFMRMQAGGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAAGEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
g614	AGSPGTGKTL LAKAAGEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLDIRGREQILNVHSHKKVPLDESVDLLSLARGTGPFGSGADLANLVNEAAL					
g614	GRFDRQVVVPLDIRGREQXLNVHSHKKVPLDESVDLLSLARGTGPFGSGADLAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201 TAAAAACTG CTCGACAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

```

```
301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCGAC TTTGTGCGAA TGTTTCGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTGCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```
a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGK AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVSVSGYLIKERTDKSTFFTNA
          |||||
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVSVSGYLIKERTDKSTFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGK
          |||||
a614      PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGK
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL
          |||||
a614      AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTL LAKAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI
          |||||
a614      AGSPGTGKTL LAKAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          |||||
a614      DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGT GPGFSGADLANLVNEAAL
          |||||
a614      GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDKSDLLSLARGT GPGFSGADLANLVNEAAL
```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGga  ATTTGCGcCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggtt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcgggtg  ttCgcgcgtc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGGtggcC  GATGCCGAGG
551 CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCGTTGTGT  CgcCGTtgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCCTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCATTTC
851 CACGCCAGTT  CGTCGAGGAA  CCAAAGCCC  GCATTGTGGC  GGGTCTGTTT
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTgttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggtCtgaAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTTCGATCA  CAGCGGGCGG  TACACTTCGA  TCGGGTCGCC  GTCGCGCAGC
1101 GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCAATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVRIR  KSGKCRKLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRRR  FRARFVQDVA  DDEAVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVSVAVAEAE  FEFDPsARDV  EFVVDDEDFE  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGGAGNFA  EEEEEFFKRS  LPFPQRFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECGLK  ASDGMVILLD  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GCGGGTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGGAT
151 AGGCGCAGGA  ATTTTCCGCC  GCGTGC GGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCT  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCCGGTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCCGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTACTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTCGC  CCGGGTGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTGTGT  CCGCCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCCTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTTCATGAA
751 CGTGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

```

801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTGGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGCATCAA CAGCGGGCGG TACACTTCGA TGGCGTCGCC GTCGCGCAGC
1101 GGC GTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNAA CKPOCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFP PRAA SISQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAAAAE FEFDP SAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECC LK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAA	CKPOCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
g615	10	20	30	40	50	60
	MWKRRRRGVGSFEEQRIDAAGK	PQCGKQAEAVARQLHA	SSSHVWQILD	RRRNLP	PRAA	
m615.pep	70	80	90	100	110	120
	SISQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIW	KSGTCRLKGL		
g615	70	80	90	100	110	120
	SMSRHCATSSADGASSMLHS	YSRKSRVSSMTGMDSVWIS	CLSSFM	TVRIRKSGK	CR	RLKGL
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSIC	RRCXRTGFVQDIA	DDEVAVARVA		
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSIC	RRCFRFRVQDVAD	DEVAVAGVA		
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVF	QAVVSAAAAEF	FDPSAGNVEFVVDDEDF	GFDFVELCKR		
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVF	QAVVSAAAAEF	FDPSARDVEFVVDDEDF	GFDFVELCKR		
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVA	VGQGGTGDFAE	EEEEFFKXSLPFPRQFVEE	PKTRIVACLF		
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPNIA	VGQGGAGNFAE	EEEEFFKXSLPFPRQFVEE	PKARIVAGLF		
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVX	HDIFRVSVECC	LKASDGMVILLDFERV	CGALLWGR	STAGGTLR	
g615	310	320	330	340	350	360
	VFFARVAQADNHFCVR	HDIFRVSVECC	LKASDGMVILLDFERV	CGALLWGR	STAGGTLR	
m615.pep	370					
	CGRRRAAACRLX					
g615	370					
	CGRRRAAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GCGGGCGGCG CCGTGTTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGCAGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTTCGGTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTGTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCAGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDFG GFDKIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQSTGDFE EEEEEFFK*S LPFRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS	LD	RRRN	FP	PR	AA
a615	MRKRRRRGVGSFEEQRIDAAGKPCGKQAEAVARQLHAASSSSHVWQILD	RRRN	LP	PR	AA	
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXCRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXFRTGFVQDIADDEVAVARVA					
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNV	EFVVDDEDFG	GFDKIKLRKG			
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNV	EFVVDDEDFG	GFDKIKLRKG			
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFKXSLPFPQFVEEPKTRIVACLF
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615       GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFKXSLPFPQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDCVXHDFRVSVECCCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615       VFFARVAQADNHFDCVXHDFRVSVECCCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pep  CGRRRAAACRLX
          |||||:||||:
a615       CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACCTGG
101 CGTGGAATAG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CGCCCTGCC CGACGGCGAT GTTGGCTGCG TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGCGGCT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGGC CACGGcagac tattaCCGCC
401 TCGCCTCGCG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGagcaccg Ccggcaaatc gacgatgCCG
501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gcTTCTTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGaaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCACcgt ccgccgaaga
751 agtggcacaa TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTGc
801 gcctgtccaa aatctgcCaa aCGTGGcTGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgCAA CCgcttcaGc ctgctTTCCG CATTGTGGTT TGCCGGCGGc
901 atctATtCgc tgctcttcaA AGCTGccgaC ACCGCGCCG CGCCGTTTCC
951 ACATTtcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAatCTTgt
1001 tTctGGCCAA AGCATTCAA ACCGGAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFGE
51  VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIPKEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRCRRI PAGRTRHFR QMGRGNALPA QQIIQCRLKP
201 FOTAFSRFPY PSHERTQAA YPNIHPRHR RNPRFPVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPPHFD KAAHLALFFA QILFLAKAFK TGKLPIPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACCTGG
101 CGTGGAATAG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CGCCCTGCC CGACGGCGAC GTTGGCTGCG TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCACT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGGC CACGGCAGAC TATTACCGCC
401 TCGCCTCGCG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTACAGCGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCTCTG TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGGCGGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTGCGCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCGCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSGQVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRRI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPILRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQVAALAAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
g616	VWLLKPATFMNRSGQVAALAAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTDYYRLRLGIGHPGDRNLVVGVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
g616	DIQAKLGTDYYRLRLGIGHPGDRNLVVGVLNKPSEAPPANRRRCRRQIPAGRTRHHFR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQOMTRCRLKPFQACSRFPYPNSHRTQAAYPNRIHPRHRNRPRFPALRM					
g616	QMGRGNALPAQIIQCRLKPFQAFSRFPYPNSHRTQAAYPNGIHPRHRNRPRFPVARM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCPILRRNRCLARYAGTRRKIPAPIQTMPDMAXRGTSMNLPNRNFILLSALWFAGS					
g616	QHRRSTVRRRSGTMRHTCRRQIPAPVQNLPNVAGRGGMKLPNRNFSILLSALWFAGG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAAETAPPPPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAADTAPPPPHFDKAAHLALFFAQILFLAKAFKGLPIPYRSLIAFAFCFAV					
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX					
g616	GSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

1	ATGTCAAACA	CAATCAAAAT	GTTGTGCGC	TTGGGCAACC	CGGGCAAAGA
51	ATACGAACAG	ACACGCCACA	ATGCGGGTTT	TTGGTTCCTC	GACGAACTGG
101	CGTGGAATG	GAAGGCTTCA	TTTAAAGAAG	AAAAAAATT	CTTCGGCGAA
151	GTCGCCCCTG	CTACCCGTCC	CGACGGCGAT	GTCTGGCTGC	TCAAGCCGAC
201	CACGTTTCAT	AACCGTTCGG	GACAGGCGAT	TGCCGCCCTT	CGCGAGTTTT
251	ATAAAATCAA	ACCCGAAGAA	ATCCTCGTCG	TCCACGACGA	ACTCGACATT
301	CCCTGCGGAC	GGATCAAATT	CAAACCTCGC	GGCGGCAACG	GTGGACACAA
351	CGGCTTGAAA	GACATTCAGG	CAAAACTCGG	CACGGCAGAC	TATTACCGCC
401	TGCGCCTCGG	CATCGGCCAG	CCGGGCGGAC	GCAACCTCGT	CGTCGGCTAT
451	GTCCTGAACA	AACCCAGTAC	GGAA.CACCG	CCGACAGATT	GACGATTCGG
501	TCGCCAAATC	CCTGCAAGCC	ATACCCGACA	TCCCTGGCCG	CAAATGTGAA
551	GAGGCAACCC	GCTTCCTGCA	CAGCAAATGA	CCCGATGCCG	TCTGAAGCCC
601	TTTCAGACGG	CATGTTCCCG	ATTTCCATAT	CCGAACAGTC	ATGACCGAAC
651	TCAAGCAGCT	TATCCAAAAC	GAATCCATCC	CCGTTCATCGA	AGAAAACCCCT
701	GATTTCTGCT	TGTACGAATG	CAGCATCGAC	GACGCAACAT	CCGCCGAAGA
751	AGTGGCACAA	TGGCGCGACA	TACTTGCCGC	ACGCGGCGGC	AAATTCTTGC
801	GCCTGTCCAA	AATCTGCCAA	ACGTGGCTGG	ACGAGGAGGC	GGCATGAAGC
851	TGCCCGCGAA	CCGCTTTCAG	CTGCTTTCCG	CATTGTGGTT	TGCCGGCGGC
901	ATCTATTGCT	TGCTCTTCAA	AGCTGCCGAC	ACCGCGCCGC	CGCCGTTTTCC
951	GCATTTTCGAC	AAAGCAGCAC	ACCTTGCCCT	GTTTTTCGCA	CAAACTTGCC
1001	TTTTGACCAA	AGCATTCAA	ACCGGAAAAC	TTCCCATCCC	TACCCGACG
1051	CTGATGGTCT	TTGCCCTCTG	TTTCGCCCTC	TTCAGCGAAT	GCGCGCAGGC
1101	ATGATTGTTACC	GCAACGAGAA	CCGGCAGTTT	GGGCGATGTT	CTTGCCGATA
1151	TGGCAGGTAC	GGTTCCTCGA	CTCTTTGCCG	CCCAGCGCCG	CGACCGCCCC
1201	GACTGA				

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

1	MSNTIKMVVG	LGNPGKEYEQ	TRHNAGFWFL	DELAWKWKAS	FKEEKKFFGE
51	VARATLFDGD	VLLKPTTFM	NRSGQAAAL	AQFYKIKPEE	ILVHDELDI
101	PCGRIFKFLG	GGNGGHNGLK	DIQAQLGTAD	YYRLRLGIGH	PGDRNLVVGY
151	VLNKPSTEXP	PTD*RCRRQI	PASHTRHPCR	QM*RGNPLPA	QOMTRCRLPK
201	FQTACSRFPY	PNSHDRTQAA	YPNRIHPRHR	RNPRFPAVRM	QHRRRTIRRR
251	SGTMAHRTCR	TRRQIPAPVQ	NLPNVAGRGG	GMKLPNRNRS	LLSALWFAGG
301	<u>IYSLLFKAAD</u>	TAPPPFFHFD	KA AHLALFFA	QIWLTKAFK	TGKLPIPYRS
351	<u>LMVFALCFAL</u>	<u>FSECAQA*FT</u>	ATRTGSLGDV	LADMAGTVLA	<u>LF AARAADRP</u>
401	D*				

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKKEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKKEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
a616	VWLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
	70	80	90	100	110	120
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	QMGSRNPLPAQQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRRNPRFPALRM					
a616	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRRNPRFPAVRM					
	190	200	210	220	230	240
m616.pep	QMGSRNPLPAQQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRRNPRFPALRM					
a616	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRRNPRFPAVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300


```

m616.pep      QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPD MAXRGTS MNLPNRNFILLSALWFAGS
              |||| :||| :|||: ||||:||||:|:|:| || :||:|||| |||||:|:|
a616          QHRRRTIRRRSGT MARHTCRTRRQIPAPVQNL PNVAGRG GGMKLPNRNFSLLSALWFAGG
              250      260      270      280      290      300

              310      320      330      340      350      360
m616.pep      IYSLLFKAAETAPPPFP HFDKVAHLALFFAQIWLLTKAFRTDNRPIPYRSLMVFALCFAL
              |||||:|||||:|||||:|||||:|||||:| : |||||:|||||:|
a616          IYSLLFKAADTAPPPFP HFDKAAHLALFFAQIWLLTKAFKLGKLPYRSLMVFALCFAL
              310      320      330      340      350      360

              370      380      390      400
m616.pep      FSECAQAWFTATRTGSLG DVLADLTGAALALFTARAACRPDX
              ||||| |||||:|||||:|||||:|||||:| ||||
a616          FSECAQAXFTATRTGSLG DVLADMAGTVLALFAARAADRPDX
              370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCTGT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtcgGC
301 GCGGTGGGCT ATAcattccct gccgttgacg gGCAAATTCG GCTTTGAACT
351 GGTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTTGCGG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT TGTGCGCCCG
751 GTAGACTTTT TCGGGCTTCT CGCCGCCCTCG CTTGCCAACC ACTTTTCCCC
801 gtCCGTGCGC CATTCCGTCC GCCTGCCgat gacggtttGC gtcgGcggCA
851 TCCTCTTGgt cggCggacaA ACCGTATTCT AACACTTCTT GGGCATGAag
901 gCggTATTAA GCGTGGTGGt cgAATTTGCG ggcggactcG TTTTCCTCTA
951 TCTCGTTTAA AAACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFLVHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTLVFTFG
101 GVGYTSIPLT GKFGFELVVM MGSLLLFYT LIRQGGRLDLP HMLIGVIFG
151 ILFRSLSSL RMIDPEEFT AAQANMFAGF NTVRSELLG GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCTGT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCTCT TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TTGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTTCGGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
351 GGTCTGCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTTGTCG CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 CTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTGCGCCCG
751 GTAAGCTTTT TCGGGCTTCT CGCCGCCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTCT AACACCTGCT CGGTATGCAG

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901 GCAGTGTGA GCGTAGTAGT AGAATTGCCC GCGGACTCG TTTTCCTCTA
951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep

1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLTK
51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LOTLLVFTFG
101 GVGYSPLPT GKFGFELVVM MGSLLLFYT LIKQGGDLS RMILIGVIFG
151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
301 AVLSVVVEFA GGLVFLYLV KHKX*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASPLTGKFGFELVVM					
g619	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYTSLPLTGKFGFELVVM					
m619.pep	130	140	150	160	170	180
	MGSLLLFYTLIKQGGDLSRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
g619	130	140	150	160	170	180
	MGSLLLFYTLIRQGGDLPHMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	190	200	210	220	230	240
	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKX					
g619	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq

1 ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
51 GTGGGTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGCGCTTT CGACCCAGCT
201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTCG ATTTTGCGTT
251 TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAAC
351 GGTCTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
401 AGGGCGGGCG CGATTTGCCG CGTATGATT TAATCGCGCT GATTTTCGGG
451 ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
501 AGAATTACG GCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTAGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG

993

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751 GTAAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTTCG GCGGGACTCG TTTCTCTCTA
951 TCTCGTTTAA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLIVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLP RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

      10      20      30      40      50      60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
      |||||
a619      MPSEKNIGFMAGSSRPLWVAFALLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
      10      20      30      40      50      60

      70      80      90     100     110     120
m619.pep VGVSTQLFQTLTNNPILTPSILGFDSLIVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
      |||||
a619      VGVSTQLFQTLTNNPILTPSILGFDSLIVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
      70      80      90     100     110     120

      130     140     150     160     170     180
m619.pep MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
      |||||
a619      MGSLLLFYTLIKQGGRLPRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
      130     140     150     160     170     180

      190     200     210     220     230     240
m619.pep NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
      |||||
a619      NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m619.pep VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
      |||||
a619      VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
      250     260     270     280     290     300

      310     320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKXX
      |||||
a619      AVLSVVVEFAGGLVFLYLVLKHKXX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gttttcgCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

g620.pep
 1 MKKTLAIVA VFALSACROA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWID AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDA YIFK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

m620.seq
 1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
 451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

m620.pep
 1 MKKTLAIVA VSALSACROA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACROAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	: : : : : : : : : :					
g620	MKKTLAIVAVFALSACROAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					
	: : : : : : : : :					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
	: : : : : : : : :					
g620	GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

a620.seq
 1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
 451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

a620.pep
 1 MKKTLAIVA VSALSACROA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLT	EHNGPKAQIFLNGKP		
a620	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLT	EHNGPKAQIFLNGKP		
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMF	GYTKLPEEPK	GIRVIYVTD	MGNVTDW	TNP	NADTEWMDAKKAFYVIDS
a620	DQPVWFSTIKQMF	GYTKLPEEPK	GIRVIYVTD	MGNVTDW	TNP	NADTEWMDAKKAFYVIDS
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMGAEDALP	FGNKEQAEKFA	KDKGKVVGF	DDMPDTYIFKX		
a620	GFIGGMGAEDALP	FGNKEQAEKFA	KDKGKVVGF	DDMPDTYIFKX		
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  ccgctgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCC  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCCG  CGTTGCCTGC
301 GGCTTGGAAT  CGATGGTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTTG  CTAAGAAAGT  CCGTACCGAT
451 ACCGCTGTGC  GCGAAAATTC  GGTTCGATG  GCTTCCGCGT  CCGTCAAGTT
501 GCGGGAACAG  ATTTTCCCG  ACATCGGCGA  TTGAACGTA  TTGTTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCCAGCTGA  TGACGGTTGC  CAACCGGACG  CTGGCGCGTG  CACAGGAGTT
651 GTCCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTCAAC  GGCGAGCCAG
751 CTTCCGATAG  TCGGCAAAAG  CATGGTCGAA  CGCGCATTGA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTCATG  TTGACTTGCG  CGTGCCGCGC  GATATTGAAG
851 CGGAAGTCGG  CGATTTGAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCACATCG  TCCAAAGCGg  caaggaggca  aggcagaaag  ccgccgcCgc
951 cgccgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTTGTC  AGGCAGCAGC
1001 AGGGCAGGCA  GagcgttcCG  CTGATTAAGG  CCTTGCGGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAAAATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaaCGGCG  GAAGaggttt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGGCGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGAt  tatcatttGG  ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MOLTAVGLNH  QTAPLSIREK  LAFAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGQIKDAV  RAAQEQESMG  AKLNALFQKT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEQ  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLPAILHDY  DVVVSSTASQ
251 LPIVGKGMVE  RALKQRQSMP  LFMLDLAVPR  DIEAEVGDLN  DAYLYTVDDM
301 VNIQSGSKEA  RQKAAAAAET  LVSEKVAEFV  RQQQGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLERLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHAQAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTGCG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAAG  CTGGCGTTTG  CCGCCGCCGC  CCTGCCATAA  GCCGTCGCA
101 ATCTTGCCCC  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCCG  CGTCGCCTGC

```

```
301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAACTC GGTTCATG GCTTCCGCTT CCGTCAAATT
501 GCGGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCCACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAAG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGATTGGC AGTGCCCGGT GACATTGAAG
851 CGGAAGTCGG CGATTTGAAT GATGCCATATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGCAGGCA GAGTGTCCCC TTGATTAAAG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGG GGAAGAAGAT
1201 AAAGATTGGT TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```
1  MQLTAVGLNH QTAPLSIREK LAFAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPVVGKGMVE RALKQROSMPL FMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	130	140	150	160	170	180
	RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLTMVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQROSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQROSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLRLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLRLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CCGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACCT GGTTCCTCAT GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGC GACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCATATC TTTATACGGT GGACGATATG
901 GTC AATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAACLP EAVRNLAARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHA FRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQE QESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSIQ LTNKLHLSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*

m622/a622 98.1% identity in 415 aa overlap

10 20 30 40 50 60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLAARSNAATEAVILSTCNRTELYCVGD
a622 MQLTAVGLNHQTAPLSIREKLAFAAAACLP EAVRNLAARSNAATEAVILSTCNRTELYCVGD
10 20 30 40 50 60

70 80 90 100 110 120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHA FRVACGLDSMVLGEPQILGQIKDAV
a622 SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHA FRVACGLDSMVLGEPQILGQIKDAV
70 80 90 100 110 120

130 140 150 160 170 180
m622.pep RVAQE QESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
a622 RVAQE QESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
130 140 150 160 170 180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatctTTtgg CattTTCccc aacnctggtg ggtcGGGGCG
301 GTTTCATCGG TTTTGTGTTT CCTTGTCacC ATacggatgt gGcacAGacC
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep

```

1  MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWHRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
51  TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CTGCGCTGAT AATGTTTGG CAGTTTCCC AACGCTGGTG GGTGCGGGCG
301 GTTTCATCGG TTTTGTGTTT CCTGTGCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep

```

1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGGISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

```

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g624          HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1   ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTTGGG
51  TATCATCGGC ATTTTGTGCG CGCTGTTGCC GACCACGCCG TTCGTAAGTC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCCG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
301 GTTTCATCGG TTTTGTGTTT CCTTGTCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1   MIRYLLIACG CISLLGLIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/a624 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624          MIRYLLIACGCISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV
              10      20      30      40      50      60

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624          HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1   ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1   atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtctTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtAA

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1   MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA

```

1000

51 VLSLGVPFKS P QTKMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGCG AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACC
301 AAATGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS P QTKMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	P QTKMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	P QTKMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS P QTKMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	P QTKMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	P QTKMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCGGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTCTCC TCGGCATCTT
201 CATCAACATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCCTG TTTTATTcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gCAACgcac cgaactTCAT

1001

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGcCg actTTCTTcc
 551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CATcgTACAT
 601 ACCCTcgtCT TTTTcgTttt cAAACTACTg taa

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

g627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

m627.seq
 1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCTATCG CGAAGTGGGC AAACCTCTTC TCGGCATCTT
 201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCCGCAT TCTTGATAA
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
 401 CCTTGATGAC GGGTACCCTG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTCTCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

m627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLIFFVFKLL *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	:					
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGSMVFMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGPLFHSLLAVSMGSMVFMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGSMVFMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGPLFHSLLAVSMGSMVFMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1   ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GCGGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTG TTTTATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAAGTTTAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1   MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGSMVFMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGSMVFMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
a627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTGAGCGGCG TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTTCGGCGC CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNTNRP
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GGTTCGGCGC CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRP
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLNTNRPRLKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRLNTNRPRLKSSAASLMM				
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

a628.seq
 1 ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
 101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
 151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGC GAACGGC TCGGCATCGA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGG
 351 TTCGGGCGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

a628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
 51 LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
 101 DWIRLRTSS PLKFANASGA *

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS DGTSAP AALQTWILRSVKRLNTNRPLKSSAASLIM					
	:					
a628	MCVPLKPAGCGPPNSCVSMLAAFS DGTSAP AALHTWILRSVKRLNTSKPRLKSSAASLIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSAVHKPDWIRLRTSSPLKFASASGA					
	: :					
a628	TTGSAASGLVSIALTKMANGSASTAGILLNGRVRSAVHKPDWIRLRTSSPLKFANASGA					
	70	80	90	100	110	120

m628.pep X
 |
 a628 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

g629.seq
 1 ATGACTGCca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
 51 ggtatTGTTT GCCGTCAGcc tGtcggTCGG cattgccgaT TTCCGCTGGT
 101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
 151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc
 201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta
 251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgtctct gAtgtccctg
 301 ctgctgcctg CcgGccgct gccggtcaAA ATGTCGGtag Ccgccgttgc
 351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac
 401 cgacggcgca gctgatGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
 451 GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAAT
 501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
 551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CGGTGTTTGC CTACCTGATT
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
 651 GGGTTTGAAC CGGACGGCGG TGTGTGGTC GGGTTTGATT ATTGTGGCAC
 701 TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATTCC GTTATCGGG
 751 CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA
 801 AAGCCTGCCT GCGGTCGCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG
 851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG
 901 GTTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

g629.pep
 1 MTAKPFSLNL ANLLLPVLF AVLSVGIAD FRWSDVFSLS DSQQVMFISR
 51 LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGILLMSL
 101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGXIFGGV

```
m629.seq
1   ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51  GGTGTTGTTT GCCGTGACGC TGTGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CTGATGTGTT TCTACTGTCC GACAGCCAG AGGTCATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCATG TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTTGTC GAACCGTCGA
251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCTG
301 CTGCTGCCGG CCGCGCCGCT GCCGCGGAAA ATGTCCGGTT CCGCCGTTCG
351 CGCGTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CTTTGGTCTG GGTATTATTT CGCGGTGTG
451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GGCAGTTTGG CCGTGTTCGC CTATCTGATT
601 CCCGACCGGC TGACGATTTT GGGCTTGGGC GAAACGGTAA CGCTGAATTT
651 GGGTTTGAAC CGCAGCGCGG TGGTGTGTCG GGGTTGATTT ATTTGTGGTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTTGCGCCA
801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
851 ACATTATCCG ACGCGTGATT GTGTTTCCGT TTGAAATTCC GGTCTCTACG
901 GTTTTGTGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCTATG CCGCTCTGA
```

m629.pep

1	<u>MTAKPFSLNL</u>	<u>TNLLLAVLF</u>	<u>AVLSVGVD</u>	<u>FRWSDVFSLS</u>	<u>DSQQVMFISR</u>
51	<u>LPRTFAIVLT</u>	<u>GASMAVAGMI</u>	<u>GMILMRNRFV</u>	<u>EPSMVGASQS</u>	<u>AALGLLLMTL</u>
101	<u>LLPAAPLPK</u>	<u>MSVAAVAALI</u>	<u>GMLVFMLLR</u>	<u>RLPPTAQLMV</u>	<u>PLVGIIFGGV</u>
151	<u>IEAVATFIAY</u>	<u>ENEMLQMLGV</u>	<u>WQQGDFSSVL</u>	<u>LGRYELLWIT</u>	<u>GGLAVFAYLI</u>
201	<u>ADRLTILGLG</u>	<u>ETVSVNLQSL</u>	<u>RTAVLWSGLI</u>	<u>IVALITSLVI</u>	<u>VTVGNIPIFI</u>
251	<u>LVVPNIISRL</u>	<u>MGDRLRQSLP</u>	<u>AVALLGASLV</u>	<u>LLCDIIGRVI</u>	<u>VFPFEIPVST</u>
301	<u>VFGVLGTALF</u>	<u>LWLLLRKPAY</u>	<u>AV*</u>		

Homology with a predicted ORF from *N. gonorrhoeae*

m629.pep	10	20	30	40	50	60
	MTAKPFSNLNLTNLLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
g629	MTAKPFSNLNLANLLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
m629.pep	70	80	90	100	110	120
	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLLMTLLLPAPLPAKMSVAAVAALI					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLLSLLLPAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
m629.pep	130	140	150	160	170	180
	GMLVFMLLIRRLPPTAQLMVPLVGIIFFGGVIEAVATFIAYENEMLOMLGVWQQGDFSSVL					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFFGGVVEAVATFFVAYEFEMLOMLGVWQQGDFSSVL					
	130	140	150	160	170	180
m629.pep	190	200	210	220	230	240
	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					

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g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GCGCGGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTTGTC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCT GATGTCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTGGACGGT
551 ATGAAGTGT GTGGGCAACG GGGATTTTGG CTTTGTGTC CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTATGGCTTT TGTAAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSNLN TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMMILIR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

m629/a629  95.7% identity in 322 aa overlap

           10      20      30      40      50      60
m629.pep  MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMV GASQAALGLLMTLLLPAAPLPAKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180
           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  gtacaacgtc GCGCACAGG CATTCGGTGC CTTAACGCCG GATTtgctgc
101 aacaaagcat cgcccacgac ggcaattacg ccctcgcaa cgctttgggc
151 atcaatatgt ccccgaaGc gggcgtgtTg ggcaaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTATTGTG GGcggcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCGGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCGG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg tctgacacc aaagctatgt ttgctatgca
801 ctggtacat ggcacttggt GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALT P DLLQOSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFA VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLNFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GCGCGCAGG CATTCGGTGC GTTAACGCCG GATTTGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATT ACGCGACTGT ATTTGTTGTG GGCGGTTTCT
251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAc ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCGG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTCTTGCGC CATTATTGCC GCGGTGATGA TCGGTATGAT TGCGATGTCT
751 TCGCTGTPCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC

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801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCCG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
 1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

m630.pep	10	20	30	40	50	60
	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	10	20	30	40	50	60
	MMILVWLALFPPMFYGMYNVGAQAFGALTPDLLQOSIAHDGNYALANALGINMSPEAGVL					
m630.pep	70	80	90	100	110	120
	DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	70	80	90	100	110	120
	GKMLFGAIYFLPIYATVFIVGGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
m630.pep	130	140	150	160	170	180
	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
g630	130	140	150	160	170	180
	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
m630.pep	190	200	210	220	230	240
	QWAAHGADGLKNAVGTQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	190	200	210	220	230	240
	QWAAHGADGLKNAVGTQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA					
m630.pep	250	260	270	280	290	300
	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYHHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
g630	250	260	270	280		
	GVMIGMIAMSSLINFIGSDTKAMFAM---HLVHGTWWKDDYHSLYIK.					
m630.pep	310	320	330	340	350	
	YGALIGVMCVLIRVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GGCGCACAGG CATTCGGTGC GTTAACGCCC GATTGTGCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCCGGCG
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GCGGTTTCT
 251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCTGT TCTTCGCTA CCCTGCCAAC TTGAGCGCG ATGCGGTTTG
 501 GACGCGGTT GACGCTATT CCGCGCAAC CGCGCTGGCG CAATGGGCGG
 551 CACACGGTGC AGACGGCCTG AAAAAGCCCA TAACCGGTCA AACCATCACT
 601 TGGATGGATG CGTTTATCGG CAACTGCCC GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCa ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGCAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLEMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMLLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

m630.pep	10	20	30	40	50	60
	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIANDWHYALANALGINMSSEAGVL					
	10	20	30	40	50	60
m630.pep	70	80	90	100	110	120
	DKMLFGAIYFLPIYATVFVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
a630	GKMLFGAIYFLPIYATVFIVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	130	140	150	160	170	180
	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	190	200	210	220	230	240
	QWAAHGADGLKNAVITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	250	260	270	280	290	300
	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLEMATDPVSASFTNVGKWW					
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLEMATDPVSASFTNVGKWW					
	250	260	270	280	290	300
m630.pep	310	320	330	340	350	
	YGALIGVMCVLIRVVNPAYPEGMMLLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
a630	YGALIGVMCVLIRVVNPAYPEGMMLLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTCCGAA GACAGGGCAT AGCCTTTTCG
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGAGGA

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
 401 GCAGCATTC AAGGATAAGA CAAGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSQYR KMVVFVFIQI HDDGDFQLRE LFERQGIQFR
 51 LKTQIGHNAP HILKRRHLF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPRFPTLQF DFSVNNRIIV KHRCSIQTIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
 201 GCATCTGCTC CTTATCCAGT TTTTCAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGAGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIQFR
 51 FKTQIRHNAP HILKRRGHLI LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIQFRFKTQIRHNAP					
g635	: : : : : : : : :					
	10	20	30	40	50	60
m635.pep	70 HILKRRGHLI LIQFFXHVLF RQLLPVKIVQ KRRHRSRPAG KIQILLYNIE IAPFFPTLHF	80	90	100	110	120
g635	: : : : : : : :					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	:					
	130	140				
	DFSVNNRIIVKHRCSIQTIRQGSVPDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIQFR
 51 LKTQIRHDAP HILKRRHLL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10 20 30 40 50 60

1011

```

m635.pep  MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNP
a635      MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDAP
           10      20      30      40      50      60

           70      80      90      100     110     120
m635.pep  HILKRRGHLILLIQFFXHVLFRLQLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635      HILKRRGHLILLIQFFXHVLFRLQLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
           70      80      90      100     110     120

           130
m635.pep  DFSISNRIIVDX
a635      DFSISNRIIVDX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcccACGG
201 AAATATTGCC GCTGacttcg ctgtcgtTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTCACG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAAT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGCGAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCGCGCGCG TGTACGGCTA TGGTACGCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGCGAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCGCCCGG
751 GCGCGGGGCA AAAATTTCGG CAAGGTGTGC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCCGAACAA AATAAAGCAT CATCAAATG TGCTGTGTTT
951 TATAGCGAAA CCGCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGNUAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIVVFNQG ARGGFFEINT GIHCWQAHG TGNGQVAERY
201 VRRVYGYGTP ALVFFDGGT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201 AAATATTGCC GCTGATTTCT CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACG
401 CGCAAAAGTC CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGCGAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGCGCGC TGTACGGCTA TGGTACGCC GCTCCTGTGC CCTTCGATGG
651 TTGCGGAACG GTCGCGAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep
 1 MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVI VDGETQIAEA VVFIGVVRAG
 101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
 151 RTMQIYADRI IQNIVVFNQG ARGSSFEINT GIHCGQAHTG TNGGQVAERY
 201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
 251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVG	IIGKYALACL	VDNVVVNIGI	VDIVEHNALI	AAADGDIVEY	FEPLGKHQHI
g638	MIGGQFIVVG	IVGKNALARF	VDNVVVNIGI	VDIVEHDALI	AAADGDIVEH	FEPFGKHQHI
	10	20	30	40	50	60
	70	80	90	100	110	120
m638.pep	AHIVAHGNIA	ADFAVVGVI	VDGETQIAE	AVVFIGVVR	AGIGKNAVPP	FGNVVADDLRTG
g638	AHIVAHGNIA	ADFAVVGVI	VDGETQVAE	AVVFIGVVR	AGIGKNAVPP	FGNVVADDLRAG
	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	CVPNGNAVAL	LVHAQSRVAD	DFILAHHRIG	RTMQIYADRI	IQNIVVFNQG	ARGSSFEINT
g638	RVPNGNAIAA	LIHAQGRIAD	DFILAHHRIG	RTMKVYAERI	IKNIVVFNQG	ARGGFFEINT
	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	GIHCGQAHTG	TNGGQVAERY	VRRVYGYGTP	PAPVAFDGC	CTVGRPFNR	NRFVNVKFGFIYA
g638	GIHCWQAHTG	TNGGQVAERY	VRRVYGYGTP	ALVPFDGCG	TVGRPFNRN	RFDIKFGLIYA
	190	200	210	220	230	240
	250	260				
m638.pep	GSQFERIARP	GAGKCGIPIS	IIGSX			
g638	GSQFDRIARP	GAGKNFGKV	VLRGNVDDG	CCRCRLKNA	AAGGKYQHGL	QPYTERGCVHSVPLF
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq
 1 ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51 TGCCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
 101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
 151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
 201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
 251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGTGGT
 301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
 351 GCGGCCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTCCAGG
 401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
 451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAATA TTATTGTGTT
 501 CAATCAGGCG GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
 551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
 601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCCTGTCT CCTTCGATGG
 651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
 701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
 751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep
 1 MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVI VDGETQIAEA VVFIGVVRAG
 101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
 151 RTMQIDADRI IQNIIVENQ ARGSSFEINT GIHCGQAHTG TNGGQVAERY
 201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFLIYA GSQFERIARP

1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLVDNVNVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVNVNIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
m638.pep	AHIVAHGNIAADFVAVGVHIVDGETQIAEAVVFVGVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFVAVGVHIVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRAG					
	70	80	90	100	110	120
m638.pep	CVPNGNAVAALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIVVFNQARGSSFFEINT					
a638	RVPNGNAIAALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQARGSSFFEINT					
	130	140	150	160	170	180
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCGTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRVGRPFNRNRFVDVKFGLIYA					
	190	200	210	220	230	240
m638.pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIIDSX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCTG GTTGAACACA ACAATATTTT TGATAATTTC TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCCAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAA TATGTCAGTA CGCGCTTCTT CACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTTCCTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGMV LMFSERLKVF DNIAGVSRD*
151 GIMLNIVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTCCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTTC GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGA
201 CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCCAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTACAAAAA CAACCGCTTC
301 AGCGATTGTC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGCGCGC TTTCCCGCCG TTCTGCCTGG CCGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCGATCGG
1001 AATGGGGCAG GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAFG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMGGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLVNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRENG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIOTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWNAFGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWNAFGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGGYVLMFSERLKVFVFNIAVGSRDQXGIMLVNYSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVFVFNIAVGSRDQXGIMLVNYSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSGDSAYRPGIIDIQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNGIIDIQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEAETQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```
1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AACTGCCCC
51  GCGGCCCCTG ATTGAACACA ATAATATTTT GGATAATTCTG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGAA
201 CCGCCCCGGC GCGCAGGTCG TCGGCAACGA TATTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAAAC CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGGT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGCAAT TCCTTTATCA ACAACGAAAG
651 CCAGTCAAA TACGTACGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCAGCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAA TTTCCCGCCG TTTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CCGCAGTTGG
1001 AATGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG
```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```
1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNA PG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMGMVY LMFSERLKVF DNIAVGSRDQ
151 GIMLNYVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPN G IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF PAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*
```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a639-1.pep	NGVTVWNA PGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNA PGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a639-1.pep	ISVGNMGMVYLMFSERLKVF DNIAVGSRDQGIMLNYVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGMVYLMFSERLKVF DNIAVGSRDQGIMLNYVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTA AIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGF GDSAYRPN GIIIDQIIWRAPVSRLLMNSPAISIVKWAQAF PAVLPGGVV					
m639-1	NSAFDLNGDGF GDSAYRPN GIIIDQIIWRAPVSRLLMNSPAISIVKWAQAF PAVLPGGVV					
	250	260	270	280	290	300
	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTCGA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCAGCGT
501 GGCGCCGGGC GACATCATCA GcggTGCGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGAAGC
651 CGCGCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCAG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTGTGA TGTTCCTTG GTCAGCCAGC CTTCCATCGG TAAAGGCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACC CGGGCA
951 GCAGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCGCGGTT TTAAGAAGT TTCTTGGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
201 GSDKALQAS ASDVREAAPA SETRFRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGD PD FIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVRGGI FDRIEMIQGE
351 NSFRFTDAQH ERVVELSAAD APRFKEVSWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGTTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

```

m640.pep      10      20      30      40      50      60
MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFLTAALPAYAERLPDFLAK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g640          10      20      30      40      50      60
MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFFVFLTAALPAYAERLPDFLAK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
70      80      90      100     110     120

```

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
               130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

               10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
               |||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
               10      20      30      40      50      60

               70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||
a640          DGTIAGAKLVDHHEPIMLIGIPH
               130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGCGTTTTG CAGAAAGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG GTTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggttT Gcacggcgctc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTCTTCGG CGGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGCGGgc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTGCGCGC GTTCGTAATC GACGAATCTG

```

1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGAGCGG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCTGCCAGT ATTTGCGGGC
1051 GttgACGTAA ATGTTtgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCgcgcgcg gaggtTtcggt gttcggtaAc gccccaacgg
1151 cggcttttcgc ctTTGAAAT CATGTCCAAA CCTGTGCGA CTTGCgtctt
1201 gccgcggaac tCTTGAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEGC
51 GVVFVLLYED KKS GDDFADE DFLQAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLV FVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEF LQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVC FGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGF GFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGCCGAT GTCGTT CAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCCGAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGGCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATTT GATGTGTTG CCGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAAACGCG GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGA CTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTTG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CTTTGA AAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATGCGCGAA CTCTTGCA GT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICPLPA ISAVQYIFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADV SFQI FKDVFNHVR HADQLQAAAD KDLERAQTG
251 SVALGEFHFG GCRHFGIDAV DGVT DGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFV GLHFACNRRR
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VQEGCGVFVRLYED		
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VQEGCGVFVFLLYED					
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN					
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEF	LQHLRGG					
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGVWSAFKTLRAQEF	LQHLRGG					
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKNLGNLMAAPDFAAFV	IDEFDV	VADVS				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFV	IDESD	IVADIS				
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHAVRHADQLQAAADKDVLERAQ	TGSVAL	GEFHHG	CRHFG	IDAVD	GVTDGA	
g642	VQVVKDVFNHAVRHADQLQAAADKDVLERAQ	TGSVAP	GEFHHG	CRHFG	IDAVD	GVTDGA	
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFR	GDVNG	LVS	DI			
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFR	GDVNG	LFVGI				
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQ	HQRAFD	AGTQR				
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVQTLCDLRFIAELLQRLQ	HQRAFD	AGTQR				
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1   GCCTGCCGCC GTATTTGCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCGGAT GTCGTTCAAG AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGCGCAG GCATCGGTCA GGGTGTGTT CTGCAGGAAG CTGCGGATGT
201 CTTCGGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCAGGCGCG CGTAAAGTGA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCAGCGCCG
601 GATTTTCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATCCATAA TGCCGTGCGT CATGCCGATC

```

1020

```
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G
```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```
a642.pep Length: 407
  1 ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDVLERAQTF
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRRA
351 GGFVFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP
```

m642/a642 95.8% identity in 407 aa overlap

```
          10      20      30      40      50      60
m642.pep  ACRRICPLPAISAVQYIFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
          |||||  |||||:|||||
a642      ACRRICPLSAISAVQYVFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
          10      20      30      40      50      60

          70      80      90     100     110     120
m642.pep  LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV FVQLHACFFFFGGGADKL VVNFGIKHIV
          |||||  |||||:|||||
a642      LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLV FVQLHACFFFFGGGADKL VVNFGIKHIV
          70      80      90     100     110     120

          130     140     150     160     170     180
m642.pep  RAFKNREGADVDS DIAGGVS AFKTLRTQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
          |||||  |||||:|||||
a642      RAFKNREGADVDS DIAGGVS AFKTLRAQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
          130     140     150     160     170     180

          190     200     210     220     230     240
m642.pep  RRNGMADVAVK NNLMAAPDFAAFVIDEFDV VADVFSQIFKDV FHNVRHADQLQAAAD
          |||||  |||||:|||||
a642      GRNGMADVAVK NNLMAAPDFAAFVIDESDV VADVFSQVFKGV FHNVRHADQLQAAAD
          190     200     210     220     230     240

          250     260     270     280     290     300
m642.pep  KDVLERAQ TGSVALGEFHHGGCRHFGIDAVDGV TDGAQAFGCEGFAADVC FGDEQQVDDF
          |||||  |||||:|||||
a642      KDVLERAQ TGSVALGEFHHGGCRHFGIDAVDGV TDGAQAFGCEGFAADVC FGDEQQVDDF
          250     260     270     280     290     300

          310     320     330     340     350     360
m642.pep  GEFVAFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGF GFGNTQT
          |||||  |||||:|||||
a642      GEFVAFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGF GFGNAXT
          310     320     330     340     350     360

          370     380     390     400
m642.pep  AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
          |||||  |||||:|||||
a642      AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
```

1021

370

380

390

400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAC
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCCG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagaTGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAT
351 GACCTGCGCg aGTGtTGCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1   MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCCG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCCG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1   MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLAT	IRSATLTLXRL	LAMLN RVSPST	TTRWMLAWSG	EISASPSAAL	ATRVSKRTRR
g643	MVLPLMLLAT	IRSATLTLXRL	LAMLN RVSPST	TTRWMLAWSG	EVSA	SPSAALATRVSKRARR
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCG	DAEILCSATV	SGVPMTAEMV	SSACRRRLFR	ATSCMSSSAA	CMSFWGMICA
g643	LPSAATVCCG	DEEMLCSATV	SGVPMTAEMV	SSACRRRLFR	ATSCMSSSAA	CMSFGGMTCA
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGM	AVCF	SVX			
g643	SVAVWVSDGM	AVCF	SVX			
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

a643.seq
 1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTGCGCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGCGCT TTGCCGTCGG CCGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGCGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
 351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCCGTTTG A

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

a643.pep
 1 MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTEMVSSACRRRLFRATSCMSSSAA	CMSFWGMICA				
a643	LPSAATVCCGDEEMLCSATVSGVPMTEMVSSACRRRLFRATSCMSSSAA	CMSFWGTICA				
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMAVCFVSX					
a643	SVAVWVSDGMAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

g644.seq
 1 ATGCCGCTCG AAAGGcgcGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCGGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
 201 ATTcCCCCG ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTTGCTGTT GCCCTCCTC
 301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
 351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGTGTTG CAGCCTCTGC AAGagttcgg cggcgaagcG
 451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAagcgcaaa gccgcccgttt
 501 gggcgTtacc gaaccggaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
 551 agtcctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
 601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgcaaa
 651 agagcgcaaa aacGGcaaac tcgccaagt CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
 801 GATGAAACTC TCCCGGGGCG ACGTGCCCG TTTGCGCGCG TTCCAAACA
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
 951 CGTCGATTAC GAACCGCGCG AAATCCAACG CCGCCATCAG GTTTCCGAAA
 1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtcgc GCccgTCGCC
 1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
 1101 TTAcgcCGCC GCGCAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
 1151 AACGCGGACA CCCAGCCGCG AATATCGCCA TCGATATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCCAACGA TATGCTTTAT GCCGAAATT ACGACAGTT
 1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
 1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgtt tgCCGCGGTT
 1351 GCCcgcGacT ACGCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

1023

1451 TCGCCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCTTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEYI DEQTIYVNAA
 201 KYWQGNQSQD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHRQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGIK LDKNQTLDDA VQTDVRFVA
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCGCGCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
 201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCTTGG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTGG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT
 501 GGGTGTACC GAACCCGAAA CCTCCGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCGCT
 801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTTACCG CAGCCGCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCGAGAG
 1001 TTCTTTACCG CTACGCTGCG CATTCGTTT CGCCTGTTGC CCCCCTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAAATGT TGCAAAAACCT CTTGGGTGCG AAGGGTTTGG
 1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAATT
 1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
 1351 GCCCGCGACT ACACTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCGTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCCGCCGACT CTTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSEPADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA
 201 KYWQGNQSQD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDDR LQTDARFAAV
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

	10	20	30	40	50	60
	70	80	90	100	110	120
m644 . pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRRKGSQFEIQEVLRI					
g644	LKHIESAFPRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKHGGRKGSQFEIQEVLRI					
	130	140	150	160	170	180
m644 . pep	AGHYGVVPTLRTGIEGALVLQPLQEFGEAQAQGLEMI FKGE GGLGVTEPETSGAAIA					
g644	AGHYGVVPTLRTGIEGALVLQPLQEFGEAQAQGLDMIFKGESRR LGVTEPETSGAAIA					
	190	200	210	220	230	240
m644 . pep	REMQSYEYIDGQTIYVNAAKYWGNSQSD FLLVAAKERKNGKLAKVIDLLLVPKTYIRC					
g644	REMQSCYEYTDQTIYVNAAKYWGNSQSD FLLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	250	260	270	280	290	300
m644 . pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	310	320	330	340	350	360
m644 . pep	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
g644	EYILDNLNRYVRNDIRFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPN DMLYAEIYDQFVRA					
g644	TLATEYTYAAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPN DMLYAEIYDQFVRA					
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLTDACALQKVFI					
g644	TAEKEAGIKLDKNQTL DAVQTDVRF AAVARDYAL PEDIRSFLOEHTLTDACALQKVFI					
	490	500	510			
m644 . pep	GKIIARLFVVFVQAKHEDTAAFLNDIRKDILD CRYCGX					
g644	GKIIARLFVVFVQEEHEDTTAFLNDIRKDILD CRYCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644 . seq
1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGCGCG GCGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTTCAGT CAACGCCCGC
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCAGAGCG ACGTGCCGG TTTGCGCGCG TTCCAAAACA

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1025

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851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACAGTT
1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```
a644.pep
 1 MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKYGGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYT DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIFIRSRL QLIGMTHGIM
301 EYTLNLERV VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*
```

m644/a644 97.3% identity in 517 aa overlap

```
              10      20      30      40      50      60
m644.pep      MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644           MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
              10      20      30      40      50      60
m644.pep      LKHIESAFRRIFS DGIDLMRYLPEDKWLALKQAGLLLPFLDKYGGGRKGSQFEIQEVLRI
a644           LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKYGGGRKGSQFEIQEVLRI
              70      80      90     100     110     120
m644.pep      LKHIESAFRRIFS DGIDLMRYLPEDKWLALKQAGLLLPFLDKYGGGRKGSQFEIQEVLRI
a644           LKHIESAFRRIFS DGIDLMRYLPEDKWLALKQAGLLLPFLDKYGGGRKGSQFEIQEVLRI
              70      80      90     100     110     120
m644.pep      AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMI FKEGGGGLGVTEPETSGAAIA
a644           AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGLGVTEPETSGAAIA
              130     140     150     160     170     180
m644.pep      AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMI FKEGGGGLGVTEPETSGAAIA
a644           AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGLGVTEPETSGAAIA
              130     140     150     160     170     180
m644.pep      REMQSYEYIDGQTIYVNAAKYWQNSQSD FLLVAAKERKNGKLAKVIDLLVPKTYIRC
a644           REMQSYEYTDGQTIYVNAAKYWQNSQSD FLLVAAKERKNGKLAKVIDLLVPKTYIRC
              190     200     210     220     230     240
m644.pep      REMQSYEYIDGQTIYVNAAKYWQNSQSD FLLVAAKERKNGKLAKVIDLLVPKTYIRC
a644           REMQSYEYTDGQTIYVNAAKYWQNSQSD FLLVAAKERKNGKLAKVIDLLVPKTYIRC
              190     200     210     220     230     240
m644.pep      ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
a644           ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
              250     260     270     280     290     300
m644.pep      ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
a644           ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
              250     260     270     280     290     300
m644.pep      EYILENLERVVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQHMEANIVK
a644           EYTLNLERVVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQHMEANIVK
```

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a644	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVVFQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG  TGTGGCGTT  GGGGATGTCG  ATGCCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACATTGA  ATCTTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCACGC  AGTTGTCCGT  GCGCCACGCC  GATACGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCGCGC  ATATTCTCAA  TCGTATCTAC
201 TTCATTGTGC  AGGAAAata  CCTGCTCTCC  GCGTTGAGT  TCGCGCAACA
251 CCGCTTCGCG  CACGCTGCCT  TCGCTGAACG  GTTTGACAAA  GGTTTTCACG
301 GCGAGGCGGC  GGCTCGGTGC  AGTGGTAATC  AGCGAGAAGT  CGCGCAGACC
351 TTCGAGCGCC  ATGCTGAGGG  TGGCGGAAT  CGGCGTGGCG  GTCATGGTTA
401 GGATGTCGAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGTCGCACG
451 CCGAAGCGGT  GTTCTTCATC  GATAATCAAT  AAACCTAAGT  TTTTGAATTT
501 TATGTCGTCC  TGCACCAATT  TGTGCGTACC  GATAACGATA  TCGACAGTAC
551 CGTCCGCCAT  GCCTTCGAGC  GTGGCTTTGG  TGGCTTTGCT  GTTGTGAAA
601 CCGCAAAGGC  TGGCGACTTT  CACGGGGAAA  TCGGCGAAAC  GGTTCGGCGAA
651 GTTTTGCGCG  TGCTGCTCGA  CCAGAAGCGT  GGTCGGGGCG  AGTACGGCGA
701 CCTGTTTGCC  GCCCATCACC  GCCACAAACG  CGGCGCGAAG  GGCAGCTTCG
751 GTTTTGCCGA  AACCGACATC  GCCGCACACA  AGTCGGTCCA  TCGGCTTCGC
801 CTGCGTCAA  TCTTTAATCA  CGGcggcgat  ggcgcgcgc  TGGTCTTCGG
851 TTCTCTCGTA  G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMMVLALGMS  MPVSMMEQSS  NTLNLCKKKS  RMTCSRSSRS  SCPCATPIRA
51  SGRVSSRSR  IFSIVSTSLC  RKNTCPPLRS  SRNTASRTL  SLNGLTKVFT
101 ARRLGAVVI  SEKSRPSSA  MLRVRGIGVA  VMVRMSTLAR  RRLSCSFCRT
151 PKRCSSSIIN  KPKFLNFMSS  CTNLCPVITI  STVPSAMPSS  VALVALLLLK
201 RERLATFTGK  SAKRSKFCA  CCSTRSVVGA  STATCLPPIT  ATNAARRATS
251 VLPKPTSPHT  SRSIGFACVK  SLITAAMAAA  WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG  TGTGGCGTT  GGGGATATCG  ATACCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACGTTAA  ATCGTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCGCGC  AGTTGTCCGT  GCGCCACGCC  GATGCGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCGCGC  ATATTTTCAA  TCGTATCTAC
201 TTCATTGTGC  AGGAAAATA  CCTGCTCTCC  GCGTTGAGT  TCGCGCAACA
251 CCGCTTCGCG  CACGCTGCCT  TCGCTAAAGG  GTTTGACAAA  GGTTTTGACG
301 GCGAGGCGGC  GGCTGGGCGC  GGTGGTAATC  AGCGAGAAGT  CGCGCAGTCC
351 TTCCAACGCC  ATACTTAAAG  TACGCGGAAT  CGGCGTGGCG  GTCATGGTAA
401 GGATATCAAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGACGCACG
451 CCGAAGCGGT  GTTCTTCGTC  GATAATCACT  AAACCTAAGT  TTTTGAATTT
501 GATGTCGTCC  TGCACCAATT  TGTGCGTACC  GATAACAATA  TCGACCGTGC
551 CGTCTGCCAT  GCCTTCAGC  GCGGCTTTGG  TGGCTTTGCT  GTTGTGAAA
601 CCGCAAAGGC  TGGCGACTTT  CACGGGGAAA  TCGGCGAAAC  GGTTCGGCGAA
651 GTTTTGCGCG  TGCTGCTCGA  CCAAAAGCGT  GGTCGGAGCA  AGTACGGCGA
701 CCTGTTTGCC  GCCCATCACC  GCCACAAACG  CGGCGGCGAG  GGCAGCTTCG
751 GTTTTGCCGA  AGCCGACATC  GCCGCACACA  AGCGGATCCA  TCGGCTTCGC
801 TTGCGTCAA  TCTTTAATCA  CGGCGGCGAT  GGCGGCGGCC  TGGTCTTCGG

```

851 TTCCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep

```
1  MMMVLALGIS  IPVSMMEVQS  NTLNRCCKKS  RMTCSSSRSR  SCPCATPMRA
51  SGRVSSRSR  IFSIVSTSLC  RKNTCPPRLS  SRNTASRTL  PSLKGLTKVLT
101 ARRRLGAVVI  SEKSRSPSNA  ILKVRGIGVA  VMVRISTLAR  RRLSCSF*RT
151 PKRCSSSIIT  KPKFLNLMSS  CTSLCVPITI  STVPSAMPSS  AALVALLLLK
201 RERLATFTGK  SAKRSKAFCA  CCSTKSVVGA  STATCLPPIT  ATNAARRATS
251 VLPKPTSPHT  RRSIGFACVK  SLITAAMAAA  WSSVSS*
```

m645/g645 93.7% identity in 286 aa overlap

```
10      20      30      40      50      60
m645.pep  MMMVLALGISIPVSMMEVQSNLTNRCCKKSRMTCSSSRSRSCPCATPMRASGRVSSRSR
          |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g645      MMMVLALGMSMPVSMMEVQSNLTNLCCKKSRMTCSSSRSRSCPCATPIRASGRVSSRSR
          10      20      30      40      50      60

70      80      90      100     110     120
m645.pep  IFSIVSTSLCRKNTCPPRLSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g645      IFSIVSTSLCRKNTCPPRLSSRNTASRTLPSLNGLTKVFTARRRLGAVVISEKSRPSSA
          70      80      90      100     110     120

130     140     150     160     170     180
m645.pep  ILKVRGIGVAVMVRISTLARRRLSCSFXTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g645      MLRVRGIGVAVMRMSTLARRRLSCSFCRTPKRCSSSIINKPKFLNFMSSCTNLCVPITI
          130     140     150     160     170     180

190     200     210     220     230     240
m645.pep  STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKAFCAACCSTKSVVGASTATCLPPIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g645      STVPSAMPSSVALVALLLLKRERLATFTGKSAKRSKAFCAACCSTRSVVGASTATCLPPIT
          190     200     210     220     230     240

250     260     270     280
m645.pep  ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g645      ATNAARRATSVLPKPTSPHTSRSIGFACVKSLITAAMAAWSSVSSX
          250     260     270     280
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```
1  ATGATGATGG  TGTGCGGCGT  GGAATGTCG  ATACCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACGTAA  ATCGTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCGCGC  AGTTGTCCGT  GCGCCACGCC  GATGCGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCACGC  ATGTTTTCGA  TGGTATCCAC
201 TTCATTGTGC  AGGAAAAATA  CTGCCCCGCC  GCGTTTGAGT  TCGCGCAATA
251 CGGCTTCGCG  CACGCTGCCT  TCGCTGAACG  GTTGACAAA  GGTTTGACG
301 GCGAGGCGGC  GGCTGGGCGC  AGTGGTAATC  AGCGAGAAGT  CGCGCAGTCC
351 TTCCAGCGCC  ATACTTAAAG  TACGCGGAAT  CGGCGTAGCG  GTCATGGTAA
401 GGATGTCGAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGACGCACG
451 CCGAAGCGGT  GTTCTTCGTC  GATAATCACT  AAACCTACGT  TTTTGAATTT
501 TATGTCGTCC  TGCACCACT  TGTGCGTACC  GATAACAATA  TCGACCGTGC
551 CGTCCGCCAT  GCCTTCCAGC  GCGGCTTTGG  TGGCTTTGCT  GTTGTGAAAA
601 CGCGAAAGGC  TGGCGACTTT  CACGGGGAAG  TCGGCGAAGC  GGTTCGGCAA
651 ATTTTGCGCG  TGCTGCTCGA  CCAGAAGCGT  GGTGCGTGCG  AGTACGGCAA
701 CTTGTTTGCC  ACCCATTACC  GCCACAAACG  CGGCGCGCAG  GGCGACTTCG
751 GTTTTGCCGA  AACCACATC  GCCGCACACG  AGGCGGTCCA  TCGGCTTCGC
801 CTGCGTCAAA  TCTTTAATCA  CGGCGGCGAT  GCGGCGTGCC  TGGTCTTCGG
851 TTTCTTCGTA  G
```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

```
1  MMMVLALGMS  IPVSMMEVQS  NTLNRCCKKS  RMTCSSSRSR  SCPCATPMRA
```

1028

51 SGRSVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
 101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
 201 RERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/a645 96.9% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMVEQSN	TLNRCCCKSRMTCSSSR	SRSCPCATPMRASGSRVSSRSR			
a645	MMMVLALGMSIPVSMVEQSN	TLNRCCCKSRMTCSSSR	SRSCPCATPMRASGSRVSSRSR			
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPL	SSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSSA				
a645	MFSMVSTSLCRKNTCPPL	SSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTL	ARRRLSCSEFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI				
a645	ILKVRGIGVAVMVRMSTL	ARRRLSCSEFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI				
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALL	LLKRRERLATFTGKS	AKRSKFCAACCSTKSVVGASTATCLPPIT			
a645	STVPSAMPSSAALVALL	LLKRRERLATFTGKS	AKRSKFCAACCSTRSVVGASTATCLPPIT			
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPH	TRRSIGFACVKSLITAAMAAWSSVSSX				
a645	ATNAARRATSVLPKPTSPH	TRRSIGFACVKSLITAAMAAWSSVSSX				
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

g647.seq
 1 ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
 201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
 251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
 301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

g647.pep
 1 MQRLAADGIQ IFFVGVGDQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
 51 GFKGTGVQTE RGTVAADVTV FRQIVGVDD TDAERTAVHS RGTRGFYRIS
 101 LII*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

m647.seq
 1 ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
 201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
 251 AGCGAACGGC GGCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
 301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

m647.pep
 1 MQRLAADGIQ IFFVSVGDQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFGKGTVGQTE					
	: : : : :					
g647	MQRLAADGIQIFFVSDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFGKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVAVADTVFRQIISIVNHADAERTA AHSRGTRGFYRISLIIX					
	: : : : :					
g647	RGTVAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

```
a647.seq
1   GTGCAAAGGC  TCGTTACACA  CAGCGTCCAA  GTCTTTTTTG  TAGGTGTCGA
51  TGGGCAGTTT  GCCTTGCGAA  TAAACGGTTT  GGTTAAGAG  CAGTGCACGCA
101 CCGTATTCTT  TGGCAAGGTT  TGCCGATGCT  TTGAGCAGGT  AACTACTGTAT
151 GGCTTCAAAG  GTACGGTGCG  TCAGACCGAG  CGCGGAGCCG  TCGCTGTAGC
201 GGACACCGTT  TTTTCGCCAA  TAATACGCAT  AGTTGATCAC  GCCGATACCG
251 AGCGAACGGC  GGCCCATAGT  GGAGGTACGC  GCGGCTTCTA  CCGGATATCC
301 CTGATAATCT  AA
```

```
a647.pep
  1  VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
 51  GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101  LII*
```

```

      10      20      30      40      50      60
m647.pep  MQRLAADGIQIFFVSVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE
          :|||:::|:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a647      VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE
          10      20      30      40      50      60

      70      80      90     100
m647.pep  RGTVAVADTVFRQIISIVNHADAERTAHSRGTGRGFYRISLIIX
          ||:|||||:||||| ||:||||:||||| |||||:|||||
a647      RGAVAVADTVFRQIIRIVDHADTERTAHSRGTGRGFYRISLIIX
          70      80      90     100

```

```
g948.seq
1  ATGAACAGGC  GCAACGCGCG  GATCGAACGG  GCTGTGCGTA  TTGCAGTGAT
51  CGACGTTTTG  AATGTAGATG  GCCCGGTGCC  CGGCACGCTC  TCGCATCAGC
101 TTGGAATAACA  GGTTCGCAGC  CGGAATGATA  CGCTTGCCTA  TGTTCGGGTC
151 TTGCTCGTAT  TTCGTATAGA  GCCGCTCAA  TTCGTCCTGG  TCGGCAAAAA
201 ACGCTTCGTA  CAACCCCGAA  ACCTCGTTGG  CGGAAAACAG  CGTAATGTTG
251 CGCCCTTAA  TCAGGCGGGT  GTACAGCAG  CGGTTGATT  GCACGCCATA
301 ATCAAGCTGG  CGGATACGGT  TGTCTTCCAC  GCCCGGGTTG  TTTTCAACA
351 CCAGCAGGCT  TTCGGCTTCA  ATATGCCACA  AGGGGTAGAA  CRAAGTTGCC
401 CGCCCGCCGC  GCACGCCACC  TTGCGAACAA  GATTGACCG  CGCCCTGAAA
451 CATCTTAAAG  AAGGGAATGC  AGCCGGTATG  CCGGGCTTCA  CCGCCCGGGA
501 TTTCGCTGTC  CAGCCCGCGG  ATACGTCGG  CATTGTGCC  GATGCCCGCG
551 CGTTGGGAAA  CGTATTTCAC  AATCGCGCTG  GTAGTGGCAT  TGATGGAATC
601 CAAACTATCG  TCGATTCAA  TCAGCACACA  GCTTGA
```

g648.pap

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFOHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCCTG ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTG GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
101 IKLDTVVVFH TAVVFOHQQA FGFDMPOGVE QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLDTVVVFHTAVVFOHQQA					
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQAVIDLHAIKLDTVVFHAPVVFOHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
g648	FGFNMPQGV E QGCRAAAHATLRTFRDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
g648	DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCCTG ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTG GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCGGGA

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1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGCA
 551 CGCTGGGAAA CGTATTTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCT TCGCATTCGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCLRK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	MNRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHAALRTGFDRLKH FKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648	FGFDMPQGV E QGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACGTC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAA CATATCAGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACGTC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VOELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
 101 FRR*

m649/g649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
g649	MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60

	70	80	90	100
m649.pep	VOELRENKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX			
g649	VOELRENKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX			
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

a649.seq

1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGAAGTGGTAT CGACAACTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
 251 CCCAATGCCG GCGGGCTTAT GAGGCTTTCG ATGATTTCTG CGGCAGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

a649.pep

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VOELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
 101 FRR*

m649/a649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
a649	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60

	70	80	90	100
m649.pep	VOELRENKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX			
a649	VOELRENKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

g650.seq

1 ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
 51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
 101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
 151 TATTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
 201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
 251 CAAGCCGCAG CTATTTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
 301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCC CGGAAGCCGC
 351 CTTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
 401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
 451 GGCTTGGAAG AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
 501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatgga CTGTTCCGGC
 551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
 601 CGCGCCGTC AACCAGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
 651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
 701 TCGCAACAT TATTGCCACC CCCCATTCTT TCGGCATGAA TATCAGCGAC

1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTGAATCC TGCATTCAAC GTCCCGCGt tcatCCCCAA AAACaaacgc
901 aaacTGCTGC TTCTGTCTGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccctt tgtccgcatt accgaaccgc ccctTGCAGC
1351 AGCCGCAGCg CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pap
1  MSKLTIALT ASGLSVCPGF LYAONTSSHQ VGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAPN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPTDYSRN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1  ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCGGTTTG
51  TCGGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGTACCAGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CTGCGTATG CCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TGCGAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGCT TTATCCCCAA AAGCAAACGC
901 AAAGTCTGTC TTCTGTCTGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCCG
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pap
1  MSKLTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAPN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTDYSRN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGRFMGEVNPVLVRRHESKFIAHSYFNRVINRSRPFMYHIANEVKKRNMPAEAAALLP					
g650	LRQGRFMGEVNPVLVRRHESKFIAHSYFDRVVNRSRPFMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDTPYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDTPYRSNMPAGTVNVSIARIQPAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCFYCRTPCDSRSATSNRKTDRAVAV					
g650	ADITVAPLPQETVRTGTRSPCFYHTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

1	ATGTCCAAAC	TCAAAACCAT	CGCCCTGACC	GCGTCAGGTC	TGTCCGTTTG
51	TCCGGGTTTC	CTATACGCC	AAAACACCTC	ATCACACCAA	ATCGGTTTGG
101	CGATTATGCG	CTTAAACTCT	TCAATACTCG	ACCTGCCACC	GACAAAACAA
151	TATTTCCAAT	CCGGCAGCCT	GTGGAGCGAG	CTGCGCCAAG	GCTTCCGGAT
201	GGGCGAAGTC	AATCCCGAAC	TGGTACGCCG	CCACGAAAGC	AAATTCATCG
251	CAAGCCACAG	CTATTTCAAC	AGGGTCATCA	ACCGGAGTAG	ACCCTATATG
301	TACCATATCG	CCAACGAAGT	CAAAAAACGC	AATATGCCCG	CCGAAGCCGC
351	CCTGCTTCCC	TTATCGAAA	GCGCGTTCTG	CACCAAAGCC	AAATCACACG
401	TCCGGCGATC	GGGCCTGTGG	CAGTTCATGC	CCGCTACCGG	CAGGCATTAC
451	GGCCTGGAAA	AAACACCGGT	TTACGACGGC	AGGCACGACA	TTTACGCCGC
501	CACCGATGCC	GCACTCAACT	ATCTGCAATA	CCTCTATGGA	CTGTTCGGCG
551	ACTGGCCGCT	CGCCTTTGCC	GCCTACAAC	GGGGTGAAGG	CAACGTCGGA
601	CGCGCCATCA	ACCGCGCCCG	CGCCCAAGGG	CTCGAACCAG	CCTACGAAAA
651	CCTGCGTATG	CCCAACGAAA	CGCGCAACTA	TGTTCCCAAG	CTGCTCGCCG
701	TGCGCAACAT	CATTGCCGCC	CCCCAATCTT	TCGGCATGAA	TATCAGCGAC
751	ATAGACAACA	AACCGTATTT	TCAGGCAGTC	GAACCGGACC	GTCCGCTCGA
801	CAACGAAGCC	ATCGCCCGGC	TTGCCGGCAT	CACGCAAAGC	GAGCTGCTCG
851	CCCTAAACCC	CGCATTCAAC	GTCCCCGGGT	TCATCCCCAA	AAGCAAACGC

1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGCA ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650.pep

```

1  MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNVVPK LLAVRNIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

```

m650/a650 99.1% identity in 465 aa overlap

	10	20	30	40	50	60
m650.pep	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
a650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE					
	10	20	30	40	50	60
m650.pep	LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEAALLP					
a650	LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEAALLP					
	70	80	90	100	110	120
m650.pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG					
a650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAT					
a650	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAA					
	190	200	210	220	230	240
m650.pep	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
a650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
	250	260	270	280	290	300
m650.pep	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT					
a650	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT					
	370	380	390	400	410	420

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRXTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRXTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1   ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCGGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCGCG CTACAAGCGG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGA GGCTTGGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct cggCGAAAC CGAAGACAGT Accattgccg
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAACccgG TTCTTTGAGc
901 cgTTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgctACT ACCCGGCAAG AGCCGCATTc TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1   MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGWKLLTEKL GKVKQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1   ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTTCTATATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAGCGG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGTAAGAG TTCAATTGGT
651 TGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGGACT ACCCGAGCAA AGCCGCATTc TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1   MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

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1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
201 EGWKKLLEKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

          10      20      30      40      50      60
m652.pep  MIELDGTENKGNLGNANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          |||||
g652       MIELDGTENKGNLGNANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          10      20      30      40      50      60

          70      80      90     100     110     120
m652.pep  EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
          |||||
g652       EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
          70      80      90     100     110     120

          130     140     150     160     170     180
m652.pep  SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          |||||
g652       SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          130     140     150     160     170     180

          190     200     210     220     230     240
m652.pep  GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
          |||||
g652       GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGKRVQLVGDDLFVTNPKILAEGIEKGVANA
          190     200     210     220     230     240

          250     260     270     280     290     300
m652.pep  LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
          |||||
g652       LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
          250     260     270     280     290     300

          310     320     330
m652.pep  RSDRMAKYNQLLRIEEELAEAAADYPSKAAFYQLGKX
          |||||
g652       RSDRMAKYNQLLRIEEELAEAAAYPGKAAFYQLGKX
          310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GCGGCAAG TCCAACCTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACG GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

1038

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFPIIS IEDGMDENDW
 201 EGWKLLETKL GGVQVLVGDD LFTVNP KILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFFPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS					
a652	LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTGTATAT TTTGCCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TCTCTATGCC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCCGCGCA AGCGTTGCGC TCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCTG ATTATTTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCGACGACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

g652-1.pap

```
1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```
1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGCGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTCCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCTGAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCCGA CTGGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pap

```
1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*
```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGD KSRYS					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGD KSRYS					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMN VINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMN VINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQLVGDDLFTVNPKILAEIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
g652-1	EKLGGKRVQLVGDDLFTVNPKILAEIEKGVANALLVKVNQIGTLSETLKAVDLAKCNRYA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAYYPGK					
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCGCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTCT GGCAGGGCGG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCGACC
601 ACAGTCCGGC ACGAAGGCGG TTTGCGCCCG AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGA AGCCGAAGGC CGTCTCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCG ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGCAAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGGCAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGAANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLS NIQEFMIMPV GAKSFREALR CGAEIFHALK KLDCSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDN NDWEGWKLLT
301 EKLGGKVQLV GDDLFTVNP KILAEIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGE EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      70      80      90      100     110     120
            GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      130     140     150     160     170     180
            AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      190     200     210     220     230     240
            CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      250     260     270     280     290     300
            LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      310     320     330     340     350     360
            EKLGGRRVQLVGDDLFVTPNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGKVQLVGDDLFVTPNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      370     380     390     400     410     420
            SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
              370     380     390     400     410     420

m652-1      429
            AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

g653.seq

```

1   ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGct ttgcccAAG
101 CGGCttcggc ggctttgcCg gtgaTTTTCa TCGGTTGCAG GtcgacgaGG
151 AAaaccTGgC TTTCTGTGCG GCCGGAaacc atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGGCGC
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTttGTGG GTGGTAGTg ttACgaaGtc GCAGaAtggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

g653.pep

```

1   MAAEPMRMPE VTYGFGSGFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

m653.seq

```

1   ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```
151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGGAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG
```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```
m653.pep
  1 MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
 51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*
```

m653/g653 96.9% identity in 163 aa overlap

```
              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
g653           MAAEPMRMPEVTYGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90     100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||:|||||
g653           MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
              70      80      90     100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATRPAX
              |||||
g653           SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATSPAX
              130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```
a653.seq
  1 ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
 51 ATCATTCCGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGGTTGCGG GTAATTTTCA TCGGTTGCAG GTCACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGGAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG
```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```
a653.pep
  1 MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
 51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*
```

m653/a653 100.0% identity in 163 aa overlap

```
              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
a653           MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90     100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
a653           MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              70      80      90     100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATRPAX
              |||||
a653           SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATRPAX
```

g656.seq

1	ATGCCGCGTT	TCTCCGGTTC	GATTTCTTCG	ATGATTTCCA	TCGCGCGGAC
51	TTTtggcGCG	CCGGAGAGTG	TGCcggcagg	gAAGGTGGCG	GCGAGGATGT
101	CCATATTGGT	AACGCCCTCT	TTCAAACAGc	ctTCGACGGT	GGAACCATGT
151	TGCATCACAT	GGGAGTATTT	TTCAATCACC	ATTTTGTCCG	TGACTTTGAC
201	TTGCCTGTT	TTGCTGATGC	GTCCGACATC	GTTGCGCCCC	AAATCGATAA
251	GCATAACGTG	TTCCGCGatt	TCTTTGGCGT	CGCTTAACAA	ATCTTGTTTCG
301	TTGGCAAGGT	CTTCGGCGGG	GGTTTTGCCG	CGCAGGCGCG	TGCCGGCGAT
351	GGGCGGAGC	ATGAGTcat	CGCGTTCGCG	CGCGACGAGG	ATTTCGGGCG
401	AGGAACCGAC	GATGTGGAAA	TCGCCGAAAT	CGTAG	

g656.pep

1	MPRFGSGSISS	MISIARTFGA	PESVPAGKVA	ARMSILVTPS	FKQPSTLETM
51	<u>CITWEYFSIT</u>	<u>ILSVTLTSPV</u>	<u>LLMRPTSLRP</u>	KSISITCSAI	SLASLNKSCS
101	LARSSAGVLP	RRRVFAMGRT	MTSSRSRRT	ISGEEPTMWK	SPKS*

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTT GACTTCTTCG ATGATTTCCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCAATGTTGGT CATGCGGTCT TTCAGACGGC CTTGCAGCTT GGAACAGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTGCG TAACTTTGAC
201 TTCGCCGGTT TTA CTGATGC GGCCGACGTC GTTGCGTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCT
301 TTGGCAAGGT CTTCCGGCGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAAGTCGTG TCGTTTCGCG TCGGACGAGG ATTTTCGGCG
401 AGGAGCCGAC GATGTCGAAA TCGCCGAATC CGTAG
```

```
m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPFS FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRIT ITSLRSRRTT ISGEEPTMWK SPKS*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTILGAPESVPAGKVAARMSMLVMPSPFRPPSTLETMCITWEYFSIT					
	: : : : : : : : : :					
g656	MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT					
	: : : : : : : : :					
g656	ILSVTLTSPVLLMRPTSLRPKSISITCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRRTRISGEIPTMWKSPKX					
	: : : :					
g656	MTSSRSRRTRISGEIPTMWKSPKX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTC TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTGTTCGG TAACTTTGAC
201 TTCGCCGTTT TTA CTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCCGGCGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTCCGGGC
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGR MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	70	80	90	100	110	120
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR					
	70	80	90	100	110	120
m656.pep	130	140				
a656	ITSLRSRRTRISGEEPTMWKSPKSX					
	130	140				
	MTSSRSRRTRISGEEPTMWKSPKSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGCGGGTta cgACCGAATT TGAaaacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATAACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTACAGGA AAAGCGTGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGT GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCcccG CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTGGCGta
751 TTGGCGGTAG AAATGTTTGT TGTGCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAACCGGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCCttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGCGCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTTCGAAAA TGGGACACTT TaccgTTTGT ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADELDYVGV

1046

251 LAVEMFVVDG THELLVNETA PRTHNSGHHT IDACAADQFO QQVRIMCNLP
 301 PADTKLLSPC CMANILGDVW QEDGGE PDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCCTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAGGAA AAGGCATGGA TACGCAAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACCTCA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
 551 TGGATTGCGC CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGCTTATTCC ATCGTCCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTGCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTGCGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCCTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDPAPAAEFA
 51 DRHLCAPFND QAALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVVCCKA EDITEASAQF LPGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADEL DYVGV
 251 LAVEMFVVDG THELVNEIA PRPHNSGHHT IDACAADQFO QQVRIMCNLP
 301 PADTKLLSSC CMANILGDVW QEDGGE PDWL PLQSHPNAL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAM	LGILGGGQLGR	MFTVAAKTM	GYKVTVLDP	DPDPAPAAE	FADRHLCA
	10	20	30	40	50	60
g657	MNTTPILPPAM	LGILGGGQLGR	MFAVAAKTM	GYKVTVLDP	DPDPNAPAA	EFAADRHLCA
	70	80	90	100	110	120
m657.pep	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
	70	80	90	100	110	120
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	130	140	150	160	170	180
m657.pep	TAPYQVVCCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
	130	140	150	160	170	180
g657	TAPYQAVCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHEL VVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXLX					
g657	TTDSDTAFQEAKKLHQSXLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

a657.seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTCGGCA	TTCTTGGCGG
51	CGGACAATTA	GGCAGAATGT	TTACTGTTGC	TGCCAAAACC	ATGGGCTACA
101	AAGTAACCGT	ACTCGATCCC	AACCCGAATG	CGCCGGCAGC	GGAATTTGCC
151	GACCGCCATT	TGTGTGCGCC	GTTTGACAAC	CAAACCGCTT	TGGAAGAATT
201	GGCAAAATGT	GCGGCTGTTA	CGACCGAGTT	CGAAAACGTC	AATGCCGATG
251	CGATGCGTTT	TCTCGCCAAA	CATACCAATG	TTTCCCCCAG	CGGCGACTGC
301	GTTGCCATCG	CGCAAAACCG	CATTCAAGAA	AAGGCATGGA	TACGCAAAGC
351	AGGCCTGCAA	ACCGCGCCGT	ATCAAGCAAT	TTGCAAAGCC	GAAGACATCA
401	CTGAAGAAAG	CATACAATTT	CTGCCCGGCA	TCCTGAAAAC	CGCTACATTG
451	GGCTATGACG	GCAAAGGCCA	AATCCGCGTC	AAAACGGTGG	ATGAAC TCAA
501	AGCCGCGTTT	GCCGAACACC	GCGGCGTGGA	TTGCGTTTTG	GAAAAAATGG
551	TGGACTTGCG	CGGCGAAATT	TCCGTTATCG	TATGCCGTCT	GAACAATGAC
601	AACGTGCAAA	CTTTCGATCC	TGCCGAAAAC	ATTCACGAAA	ACGGTATCCT
651	CGCCTACTCC	ATCGTCCCAG	CCCGACTGAG	TGCCGACATT	CAGCAACAGG
701	CGCGACAAAT	GGCGCAGCGT	TTGGCCGATG	AATTGAAC TA	CGTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCGGCGAC	ACGCATGAAT	TGTCGTCAA
801	CGAAATCGCG	CCGCGTCCGC	ACAATTCCGG	CCACCATAAC	GTCGACGCCT
851	GCGCGGCAGA	CCAATTCCAG	CAACAGGTCC	GCCTGATGTG	CAACCTGCCA
901	CCTGCTGACA	CCAAATTGCT	GAGTTCCTGC	TGTATGGCGA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGTTT	CCCCTGCAAA
1001	GCCGGCCGGA	CGCGCACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGACACTT	TACCATTTTA	AGCACCGATT	CGGACACCGC
1101	ATTTCAAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

a657.pep

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	NPNAPAAEFA
51	DRHLCAPFDN	QTALEELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLQ	TAPYQAICKA	EDITEESIQF	LPGILKTATL
151	GYDGKGQIRV	KTVDELKAAF	AEHRGVDCVL	EKMVDLRGEI	SVIVCRLNND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADI	QQQARQMAQR	LADELNYVGV
251	LAVEMFVVD	THELVVNEIA	PRPHNSGHHT	VDACAADQFQ	QQVRLMCNLP
301	PADTKLLSSC	CMANILGDVW	QEDGGEPDWF	PLQSRPDAHL	HLYGKKTAKH
351	GRKMGHFTIL	STDSDTAFQE	AKKLHQSXL*		

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAFPND					

a657	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN	10	20	30	40	50	60
m657.pep	QAALDELA	70	80	90	100	110	120
a657	QAALDELA	70	80	90	100	110	120
m657.pep	TAPYQV	130	140	150	160	170	180
a657	TAPYQA	130	140	150	160	170	180
m657.pep	EKMVDLR	190	200	210	220	230	240
a657	EKMVDLR	190	200	210	220	230	240
m657.pep	LADEL	250	260	270	280	290	300
a657	LADEL	250	260	270	280	290	300
m657.pep	PADTKL	310	320	330	340	350	360
a657	PADTKL	310	320	330	340	350	360
m657.pep	TTDSDTA	370	379				
a657	TTDSDTA	370	379				

g658.seq

1	ATGGTGGCCG	GAATTGTGCG	TGCGCGGGGC	GGTTTCATTG	ACGAGCAATT
51	CATGTGTGTC	GCCGACAACA	AACATTTCTA	CCGCCAatac	GCCGACATAA
101	TCCAATTCTG	CCGCCAagcg	TTGCGCCGTC	TGCCGCGCCT	GTTGCTGCAC
151	GTCCGCACTC	AGCCGCGcgg	gGACGATGga	atAAGCCAAg	ATGCCGTTTT
201	CGTGGATGTT	TTCCGCGGGG	TCCAAGGTTT	gcACGTTTTT	ATCGTTCAGA
251	CGGCATACGA	TCACGGAAAT	CTCGCCGCGC	AAGTCCACCA	TTTTTTCCAA
301	AACGCAATCC	ACGCCGCCGT	GTTCCGCAAA	CGCGGCTTTG	AGTTCGTCCA
351	ACGTTTTGAC	GCGGATTTGA	CCTTTGCCGT	CGTAGCCCAA	CGTAGCCGTT
401	TTCAGGATGC	CGGGCAAAAA	TTGCGCGCTT	GCTTTCAGTA	TGTCTTCGGC
451	CTTGCAAACC	GCCTGATACG	GCGCGTTTTC	CAAGCCTGCT	TTGCGTATCC
501	ACGCTTTTTT	CTGAATGCGG	TTTTGTGCAA	TGGACACGCA	TCGCGCGCTG
551	GGGAAACGT	TGGTATGCTT	TGCCAGAGAG	CGCATCGCGT	CGGCAttgac
601	gtTTTCAAAT	TCGGTcgtaA	CCGCCGCGCA	TTTTGCCAAT	TCGTCCAACG
651	CGGCCCCGTC	GTCAAACGGC	GCGCACAAAT	GGCGGTCGGC	AAATTCCGCC
701	GCGGCGCGAT	TCGGGTCCGG	ATCGAGAACG	GTTACTTTGT	AGCCCATGGT
751	TTTAGCGGCA	ACGGCAAACA	TTctgcctAA		

g658.pep

1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH

51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAOVHHFFO

m658.seq

1	ATGGTGTCCG	GAATTGTGCG	GGCGCGGGGC	GATTTCGTTG	ACGACCAATT
51	CATGCGTGTC	ACGACAACA	AACATTCTA	CCGCCAATAC	GCCGACATAA
101	TCCAATTCGT	CCGCCAAGCG	TTGCGCCATC	TGCCGCGCCT	GTTGCTGCAC
151	TCGGCGCACT	AGTCGCGCGG	GGACGATGGA	ATAAGCCAA	ATGCCGTTTT
201	CGTGGAATGT	TTCCGCAGGG	TCGAAAGTTT	GCACGTTGTC	ATTGTTCCAA
251	CGGCATACGA	TTACGGAAAT	TTCAGTGC	AAATCCACCA	TTTTTTCCAA
301	AACGCAATCC	ACGCCGCCGT	GTTCCGCAA	CGCGGCTTTG	AGTTCATCCA
351	ATGTTTTTAC	GCGGATTTGA	CTTTGCCGT	CGTAGCCCAA	CGTAGCCGTT
401	TTCAGGATGC	CGGGCAAAA	TTGCGCGCTT	GCTTCAGTGA	TGTCTTCAGC
451	CTTACAACAC	ACTTGATACG	GCGCGGTTTG	CAATCCCGCT	TGCGGTATCC
501	ATGCCCTTTC	CTGAATCGCG	TTTGTGCAA	TGCCACACA	ATCGCGGCTA
551	GGGGAACAT	TGGTATGTTT	TGCCAAAAG	CGCATCGCAT	CGGCATTGAC
601	GTTTTCAAAT	TCAGTGGTCA	CGCCGCGCA	TTTGTCCAAT	TCGTCCAAAG
651	CAGCTTTGGT	GTTAAACGCG	GCGCACAAT	GGCGGTCGGC	AAATTCTGCT
701	GCGGCGCGCT	CCGGATCGGG	GTCGAGAACG	GTTACTTTGT	AGCCCCATGT
751	TTTGGCGGCA	ACGGTAAACA	TTCGCTTAA		

m658 . pep

1	MVSGIVRARG	DFVDDQFMRV	TDNKHFYRQY	ADIIQFVRQA	LRHLPRLLLH
51	VGTQSRAGDDG	ISQDAVFVDV	FGRVSLSHVV	IVQTAYDYGK	FTAQIHHFFQ
101	NAHSAAVFGK	RGEFELQCFY	ADLTFAVVAQ	RSQFDQAGQK	LRACFSDFVS
151	LTNHLIRRLG	QSRFAYPCLF	LNAVLCNRHT	IAARGNIGMF	CQKAHRIGID
201	VFKFSGHRRR	FCQFVQSSLV	VKRRQAQMAVG	KFCCRRVRIG	VENGIFYVAHG
251	FGGKXKHA*				

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

BNSDOCID: <WO__8957280A2 | >

```

:|||||:|||||
IENGYFVAHGFSNGKHSAX
      250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

a658.seq

1	ATGGTGGCCG	GAATTGTGCG	GACGCGGCGC	GATTTCGTTG	ACGACCAATT
51	CATGCGTGTC	GCCGACAACA	AACATTTCTA	CCGCCAATAC	GCCGACGTAG
101	TTCAATTCAT	CGGCCAAACG	CTGCGCCATT	TGTCGCGCCT	GTTGCTGAAT
151	GTCGGCACTC	AGTCGGGCTG	GGACGATGGA	GTAGGCGAGG	ATACCGTTTT
201	CGTGAATGTT	TTCCGCAAGG	TCGAAAGTTT	GCACGTTGTC	ATTGTTCCAG
251	CGGCATACGA	TAACGGAAAT	TTCGCGCGCG	AAGTCCACCA	TTTTTTCCAA
301	AACGCAATCC	ACGCCGCGGT	GTTGCGCAAA	CGCGGCTTTG	AGTTTCATCC
351	CCGTTTTGAC	GCGGATTTGG	CCTTTGCCGT	CATAGCCCAA	TGTAGCGGTT
401	TTCAGGATGC	CGGGCAGAAA	TTGTATGCTT	TCTTTCAGTA	TGTCTTCGGC
451	TTTGCAAATT	GCTTGATACG	GCGCGGTTTG	CAGGCCGTGT	TTGCGTATCC
501	ATGCCTTTTC	CTGAATGCGG	TTTTGCGCGA	TGGCAACGCA	GTCGCGCTGC
551	GGGGAAACAT	TGTTATGTTT	GGCGAGAAAA	CGCATCGCAT	CGGCATTGAC
601	GTTTTCGAAC	TCGGTCGTAA	CAGCCGCACA	TTTTTGCCAAT	TCTTCCAAAG
651	CGGTTTGSTT	GTCAAACGGC	GCACACAAAT	GGCGGTCGCG	AAATTCCGCT
701	GCCGGCGCAT	TCGGGTTGGG	ATCGAGTACG	GTTACTTTGT	AGCCCATGGT
751	TTTGGCAGCA	ACAGTAAACA	TTCTGCCTAA		

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

a658.pep

1	MVAGIVRTRR	DFVDDQFMRV	ADNKHFYRQY	ADVVFQFIGQT	LRHLSRLLLN
51	VGTQSGWDDG	VGEDTVFVNV	EGRIESLHVV	IVQTAYDNGN	FAAQVHHFFQ
101	NAIHAAVFGK	RGFEFIHRED	ADLAFAVIAQ	CSGFQDAGQK	LYAFFSDVFG
151	FANCLIRRLG	QACFAYPCLF	LNAVLRDNGA	VAAGNGIMGF	GKETHRIGID
201	VFELGRNSRT	FCQFFQSGLV	VKRRTQMAVG	KFRCRRIRVG	IEYGYFVAHG
251	FGSNSKHS*				

m658/a658 75.3% identity in 259 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

g661.seq
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT GCGGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
 151 ACCGGAAAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
 201 TGCCGTGCAG ATTGCCGGCA GCGACCccga acaGATGGCG Gatgcggcgc
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
 301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
 351 CGAGccgctg gttgcCgcca tTtggaggc ggtggtcAAG GCGGCGGcgc
 401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
 451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
 501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgcGTTAC
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
 601 CGGCGACATC actTCgccgc AAAAAGCCGC CGccgTCCTC AAACAAACCG
 651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
 701 TTCCGCGATT TGAAGCATTA TGCCGAACAC GGCCTTTTAC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
 801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCAGC CAAACACATA
 851 GGCTGGTACA TCGGCGAAAT GCGCGACGGC GAACAGGCGC GCGGTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51 TGTKLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHDDQN
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
 201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
 251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTTGAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq
 1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
 151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
 351 CGAGCCGCTG GTTGCCGCCA TTTTGGAAAG CGTCGTCCGT GCGGCAGGCG
 401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
 451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
 501 CGTCC.AC GG ACGCAGCGCT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
 551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
 601 CCGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG
 651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
 701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTC GCCTGCCTT
 751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
 801 ACGCGTTTTA CCGCGACACC GCGGTGTGC GCATCGCAGC CAAACACATA
 851 GGCTGGTACA TCGACGAAAT GCGCGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHDDQN
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
 201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPFETL CRTRCFAACL
 251 EFGMRMRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVSLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSHPGLGQRRHHFAAKSRRRPQTNRRRRHDRARRARQAVVFPFRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCARHTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCGGTCTCT AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFACLE
251 EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           130     140     150     160     170     180
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPREFETL
           190     200     210     220     230     240
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHDRARRARQTVVLPREFETL
           190     200     210     220     230     240
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCARHTQTHRLVHRRNARRRDTDSX
           250     260     270     280     290     299
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCARHTQTHRLVHRRNARRRDTDSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTCTCG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTCTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTIQ FYPAWKSFFS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

```

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTTCGGAC GCAACGATTG GGTTTTTGTG
601 GATTTTTTCG GTATTTCAGAC GGCAACGATT ACCGGATTGA GCCGATTGCG
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCCTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCCTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGT GCTGCACAAG CGTTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
  1 MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
 51 KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVVF
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVTLH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
g663	10	20	30	40	50	60
	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP	RRRIGEINLAKCFPEWDEEK				
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
g663	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYASAKCLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
g663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVVFDFFGIQTATITGLSRIAALANAKVIPAI	PVREADNTVTLH				
g663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNNSVVFDFFGIQTATITGLSRIAALANAKVIPAI	PVREADNTVTLO				
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSP	DFYX				
g663	250	260	270	280	290	
	FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSP	DFYX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
  1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
 51 TCTGCCGTTT GCGTGCTGTC ACAAACCTTG TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTGGCA

```



```
151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TGGCTACCG CAACAAACAT
301 TATTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TCTGTATCT GCGCGATCAG GATTTGCGAC GCAACGATTG GGTTTTGTG
601 GATTTCTTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGC CGCAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTCTACT GA
```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```
1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHKF HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMY HOKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVVF
201 DFFGIRTATI TGLSRIAALA NAKVIPAI PVREADNTVT LH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DEFY*
```

m663/a663 96.2% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
a663	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
a663	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
a663	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
a663	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
a663	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```
1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAAGC GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGCACCCGG ATGGGCGGTC
101 GGGCTGCGT CTTGCGGGAA CTGGTCTGCG CGCAGCAGGC GGATGTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAAAC TCTTGGTCTC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAG TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTCCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcacgc gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
```

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF  FINGHGVEIV  HLLIADGAHR  MGGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKLLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEIFVSDHG
101 FNAFEIGIGG  GAAVGEDELG  VKNVQTLVFH  RAHIEIAYGD  DHENIQVIFQ
151 PEARFVPLHR  VFSTIPRQSR  PWVCPLRWCK  TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC  CGCACTACTT  CCGCGCCTTT  TTCATAACG  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TAGCTGGCGG  GCGGCACCGG  ATGGGCGGTC
101 GGGCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTT
151 GATGCGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTTCG
201 GGAACACGGT  CAGCCCTTCC  TTCAGCGAAA  GCTGGAAACA  GTCGCGGCAG
251 GTTACGCGGT  TGCCCGTCCA  GTTGTGGAAA  TACTCGTGTC  CGACCACGGA
301 TTCGATGCCT  TCGAAATCGG  TATCGGTGGC  GGTGCGGCTG  TCGGCAAGGA
351 CGAACTTGGT  GTTAAAGATG  TTCAAACCTT  TGTTTTCCAT  CGCGCCCAT
401 TTGAAATCGC  CCACGGCGAC  GACCATGAAA  ATATCCAAGT  CGTATTCCAA
451 ACCGAAGCGC  GTTTCGTCCC  ATTTTCATCG  GTTTT.CAA  CGATTCCACG
501 GCAAAGCCGA  CCTGGGGCTT  GTCCGCTTCG  GTGGTGTAAG  ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF  FINGHGVEIV  HLLIAGGAHR  MGGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEILVSDHG
101 FDAFEIGIGG  GAAVGKDELG  VKDVQTLVFH  RAHIEIAHGD  DHENIQVVFF
151 TEARFVPFHR  VFXTIPRQSR  PWACPLRWCK  TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGGRACVFGE	LVLAQQADV	FDAHGAAGAV
	:	:	:	:	:	:
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGGRACVFGE	LVLAQQADV	LDAHGAAGAV
	:	:	:	:	:	:
	70	80	90	100	110	120
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAAGYAVARP	VVEILVSDHG	FDAFEIGIGG	GAAVGKDELG
	:	:	:	:	:	:
g664	AGKLLVAEHG	QPFLQRKLEP	VAAAGYAVARP	VVEIFVSDHG	FNAFEIGIGG	GAAVGEDELG
	:	:	:	:	:	:
	130	140	150	160	170	180
m664.pep	VKDVTQTLVFH	RAHIEIAHGD	DHENIQVVFF	QTEARFVPFHR	VFXTIPRQSR	PWACPLRWCK
	:	:	:	:	:	:
g664	VKNVQTLVFH	RAHIEIAYGD	DHENIQVIFQ	PEARFVPLHR	VFSTIPRQSR	PWVCPLRWCK
	:	:	:	:	:	:
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC  CGCACCCTT  CCGCGCCTTT  TTCATAACG  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TATCGGGCGG  GCGGCACCGG  ATGTGCGGTC
101 GGACCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTT
151 GATACGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTTCG

```

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
  1 VIHPHHFRAF FINGHGV EIV HLLISGGAHR MGRTCVFGE LVLAQQADV F
  51 DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
 101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
 151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep    VIHPHYFRAFFINGHGV EIVHLLIAGGAHRMGRACVFGELVLAQQADV F DAAHGAAGAV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a664         VIHPHHFRAFFINGHGV EIVHLLISGGAHRMGRTCVFGE LVLAQQADV F DTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664.pep    AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGA AVGKDELG
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a664         AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep    VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPQRSRPWACPLRWCK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a664         VKDVQTLVFHRTTHIEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPQRSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep    TRFX
              | | |
a664         TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
  1 atgaagtGg acgaaacgcg cttcgGgttg GAAtatgact tggatatttT
  51 CATGGTCGTC GCGTAGGCG ATTTC AATAT GGGCGCGATG GAAAACAAGG
 101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
 151 ACCGATACCG ATTTCTGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
 201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
 251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
 301 CGCGCCGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
 351 GAACCAAGTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
 401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
 451 GGC GCGGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
 501 CCAAAAAGGC ATGAAGCTAT ATTTCCaaag CCACGACGGA CAGGCAAGTGA
 551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
 601 GACCAAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
 651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
 701 TGCCGCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
 751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
 801 GGGCAAACGC GCAACCGAAG CCGTGTGTGCT GATGACCGAA GCCGAACagg
 851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
 901 GGGTTCAGCG CGCCAGTGTA TCTGAAC TAT CCGTACAGCG ACGACGACCT
 951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

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1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTC A GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGAAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCAggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTTcgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAc aa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTTATCGGCT CAAGccggcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```

g665.pep
1 MKWDETRFGL EYDLDFIMVV AVGDFNMGM ENKGLNIFNT KEVLADSRTA
51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRFVSYEEMN NFYTMTVYEK
151 GAENVVMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNVFELTI KQTVPTPDM ADKQPMPIPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLN YPYSDDDLLL LAHSDAFTC WEAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROAA KQENQSYEYS PETADWRTL R
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

```

m665.seq
1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCACTTCG CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCCCGATATG ACGGATAAAC AGCCGATGAT GATCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTACAGC CGCCGGTGCA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTC A GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTC CA
1251 CTTCTGCGC AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTGCGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTGCGA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPPPTDM TDKQPMPIPV
251 KVGLLNRRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAQAOTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQQA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESTDRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLNPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

m665.pep	10	20	30	40	50	60
	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	70	80	90	100	110	120
	VVGHEYFHNW TGNRVTCRDWFQSLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDWFQSLSLKEGLTVFRDQEFSGDRAGRAVRRRIENIRLLRQHOF					
	70	80	90	100	110	120
m665.pep	130	140	150	160	170	180
	PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	190	200	210	220	230	240
	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
m665.pep	250	260	270	280	290	300
	TDKQPMPIPVKVGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMPIPVKVGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

m665.pep	310	320	330	340	350	360
	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTWRWEAAQTLYRRVAANLATLSGVELPKHEK					
g665	: : : : : :					
	310	320	330	340	350	360
	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRVAANLAALSDGIGLPKHEK					
m665.pep	370	380	390	400	410	420
	LLAAVEKVISDDLLDNAFKALLLGVPSEAEWLDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	: : : : : :					
	370	380	390	400	410	420
	LLAAVEKVISDDLLDNAFKALLLGVPSEAEWLDGTENIDPLRYHQAREALLDTLAVRFLP					
m665.pep	430	440	450	460	470	480
	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
g665	: : : : : :					
	430	440	450	460	470	480
	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
m665.pep	490	500	510	520	530	540
	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
g665	: : : : : :					
	490	500	510	520	530	540
	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
m665.pep	550	560	570	580	590	600
	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	: : : : : :					
	550	560	570	580	590	600
	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
m665.pep	610	620	630	639		
	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
g665	: : : : : :					
	610	620	630			
	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

a665.seq

1	ATGAAGTGGG	ACGAAACGCG	CTTCGGTTTG	GAATACGACT	TGGATATTTT
51	CATGGTCGTC	GCCGTGGGCG	ATTTCAATAT	GGGTGCGATG	GAAAACAAGG
101	GTTTGAACAT	CTTTAACACC	AAGTTCGTCC	TTGCCGACAG	CCGTACCGCC
151	ACCGATACCG	ATTTTGAAGG	CATCGAATCC	GTGGTCGGAC	ACGAATATTT
201	CCACAACCTGG	ACGGGCAACC	GCGTGACCTG	CCGCGACTGG	TTCCAGCTTT
251	CGCTGAAGGA	AGGGTTGACC	GTGTTCCGCG	ACCAAGAATT	TTCCGGCGAC
301	CGCGCCAGCC	GCGCCGTGCG	CCGTATCGAA	AACATCCGCC	TGCTGCGCCA
351	GCACCACTTC	CCCGAAGACG	CAGGTCCGAC	CGCACATCCG	GTGCGCCCCG
401	CCCGATATGA	GGAGATGAAC	AATTTCTACA	CCATGACCGT	TTATGAAAAA
451	GGCGCGGAAG	TGGTGCGGAT	GTATCACACC	TTGCTCGGCG	AAGAGGGCTT
501	CCAAAAAGGT	ATGAAGCTCT	ATTTCCAACG	CCACGACGGA	CAGGCTGTTA
551	CCTGCGACGA	TTTCCGCGCG	GCGATGGTGG	ACGCGAACGG	CATCAACCTC
601	GACCAATTCG	CCTTGTGGTA	CAGCCAAGCA	GGTACGCCGG	TTTGTAGATG
651	TCAAGGGCGT	CTGAAAAACA	ATGTGTTTGA	GTTAACCATC	AAACAAACCG
701	TGCCGCCAC	GCCCCGATATG	GCGGACAAAC	AGCCGATGAT	GATTCGCCGT
751	AAAATCGGGC	TGCTGAACTG	CAACGGCGAA	GCGGTGGCAT	TTGATTATCA
801	GGGCAAACGC	GCGACCGAAG	CCGTGTTGCT	GCTGACCGAA	GCCGAACAGA
851	CCTTCCAGTT	CGAAAGCGTA	ACCGAAGCCG	TCGTTCCCTC	GCTGCTGCGC
901	GGGTTTACGG	CGCCGGTGCA	TCTGAACTAT	CCGTACAGCG	ACGACGACCT
951	GCTGCTTCTG	CTCGCCCATG	ACAGCGACGC	CTTCACGCGC	TGGGAAGCCG
1001	CACAAACGCT	CTACCGCCGT	GCCGTCGCCG	CCAACCTTGC	CGCGCTTTCA
1051	GACGGCGTCG	AGTTGCCGAA	ACACGAAAAA	CTGCTTGCCG	CCGTGAAAAA
1101	AGTCATTTCA	GACGACCTCT	TAGACAACGC	TTTCAAAGCC	CTGCTTTTGG
1151	GTGTGCCGTC	TGAAGCCGAG	CTGTGGGACG	GCGCGGAAAA	CATCGACCCG
1201	CTGCGCTACC	ATCAGGCGCG	CGAAGCCTTG	TTGGATATAC	TTGCCGTCCG
1251	CTTTCTGCCG	AAATGGCACG	AATTGAACCG	TCAGGCGGCG	AAGCAGGAAA
1301	ACCAAAGCTA	CGAGTACAGC	CCCGAAGCCG	CCGTTTGGCG	CACGCTGCGC
1351	AATGTCTGCC	GCGCCTTCGT	CCTGCGCGCC	GATCCCGCGC	ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTCGAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGAGGTC GCCGCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

a665.pep

```
1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMPIPV
251 KIGLLNCNGE AVAFDYQGR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEEAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVOTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*
```

m665/a665 97.3% identity in 638 aa overlap

```
10 20 30 40 50 60
m665.pep MKWDETRFGLEYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
|||||
a665 MKWDETRFGLEYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
10 20 30 40 50 60

70 80 90 100 110 120
m665.pep VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
|||||
a665 VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
70 80 90 100 110 120

130 140 150 160 170 180
m665.pep PEDAGPTAHPVRPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
|||||
a665 PEDAGPTAHPVRPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
130 140 150 160 170 180

190 200 210 220 230 240
m665.pep QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
|||||
a665 QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDM
190 200 210 220 230 240

250 260 270 280 290 300
m665.pep TDKQPMPIPVKVGLLNRNGEAVAFDYQGRATEAVLLLTEAEQTFLEGVTEAVVPSLLR
:|||||
a665 ADKQPMPIPVKIGLLNCNGEAVAFDYQGRATEAVLLLTEAEQTFQFESVTEAVVPSLLR
250 260 270 280 290 300

310 320 330 340 350 360
m665.pep GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLATLSDGVELPKHEK
|||||
a665 GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLAALSDGVELPKHEK
310 320 330 340 350 360
```

m665.pep	370	380	390	400	410	420
	LLAAVEKVISDDLLDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
m665.pep	430	440	450	460	470	480
	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
m665.pep	490	500	510	520	530	540
	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
m665.pep	550	560	570	580	590	600
	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
m665.pep	610	620	630	639		
	CNKLEPHRKNLVKQALQIRIQEGLSKDVGEIVGKILD					
a665	CNKLEPHRKNLVKQALQIRIQEGLSKDVGEIVGKILD					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```
1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCCTGAA ACCGAACTGC ATTTGACAT  TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GGCGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTC CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCCGC
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TCGCCAGAA CCAAGTTCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAGGC GCGGAAGTGG
1151 TCGGGATGTA TATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGCGGGC ACGCCGTTT TGAAGCCGA AGGCCGCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAG CAAACCGTGC CGCCCACGCC
1401 CGATATGCGG GACAAACAGC CGATGATGAT TCCGTCAAA GTCGGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACCGCGA
1501 ACCGAAGCCG TGTTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA GCGACGCTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT
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1751 TGCCGAAACA CGAAAAATCT CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCT CAAAGCCCTG CTTTGGGCG TGCCGTCCGA
1851 AGCCGAACTG TGGGACGGCA CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGGCGGAAG CAGGAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCCG
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCAACC CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA
```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```
1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRAVRRIEN IRLLRQNFQF
351 EDAGTAPHV RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFOKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMI PVK VGLLRNNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAKAL LLGVPSEAE LWDGTENIDPL RYHQAREALL DTLAVRFLPK
651 WHELDRAAK QENQSYEYSP ETADWRILRN VCRAFLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTAHQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVG EIVGKILG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```
1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAA ACCGATTTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGAGA GGTAGGGGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGCGGCG
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGCGCGC AATTGTGTTT CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC ACAAAAAACG CTATCCCGTT
451 TTGCTTTTCCA ACGGCAACAA AATCGACGGC GCGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTT CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTTC CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCAGCG CATCGAAAAC ATCCGCTGCG TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGAGC GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCTTG CTGCGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CAGGCGGGC ACGCCGTTT TGAAGCGGA AGGTCTGCTG
1351 AAAACAATA TTTTCGAGTT GACCGTCAA CAAACCGTGC CGCCACGCG
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ACTATCAGGG CAAACCGCGC
```

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1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCTCGCT GTCGCGCGG TTCAGCGCGC
1601 CCGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCGCGCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCGCGCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCGC GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGCGCGGAC CCGCGGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTTC
2251 GTCGGCTCAA GCCGCGCAG CGACACCCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTCGAGCG CATTGCGGCG
2551 CAGGAAGCAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA
```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

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1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFS DGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHFP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPPTPDMT DKQPMMPVK VGLLRNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFLEGV EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVID
601 DLLDNAFKAL LLGVSEAE WDGAEINIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRLN VCRFVLRAD PAHIETVAEK
701 YGEMAQNMT H EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRENQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVG E IVGKILD*
```

m665-1/g665-1 96.1% identity in 866 aa overlap

```
m665-1.pep 10 20 30 40 50 60
MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV LDGSAKLLSV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 MSKTVRYLKD YQTPAYRI TELHFDIAEP QTVVKSRLTV EPQRVGEPLV LDGSAKLLSV
10 20 30 40 50 60

m665-1.pep 70 80 90 100 110 120
KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK SLMGLYASGG NLFTQCEPEG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 KINGAAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK SLMGLYASGG NLFTQCEPEG
70 80 90 100 110 120

m665-1.pep 130 140 150 160 170 180
FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFS DGRHWV KWEDPFSKPS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFS DGRHWV KWEDPFSKPS
130 140 150 160 170 180

m665-1.pep 190 200 210 220 230 240
YLFALVAGDL AVTEDYFTTMSGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL E
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 YLFALVAGDL AVTEDRFTTMSGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL E
190 200 210 220 230 240

m665-1.pep 250 260 270 280 290 300
YLDIFMVVAV GDFNMGAMENKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 YLDIFMVVAV GDFNMGAMENKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
```

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQFFEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQFFEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNMFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNMFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDMDKQPMIIPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPTPDMADKQPMIIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVLPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVAANLAALSDGIGLPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSAEALWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQAAK					
g665-1	DLLDNAFKALLLGVPSAEALWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPAAAGWRTLNRVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRAQEGLSKDVGEIVGKILDV					
g665-1	VKQELQIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTTAC ATTTTGATAT TAACGAACCG CAAACCATG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAACAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCCG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGGTCG GGGCGATTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCTGCG TCGCGCAGCA CCAAGTTCGCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGACAG GCTGTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGTTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTCGAGTT AACCATCAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAAGTCAA CGGCGAAGCG GTGGCATTG ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCAATC GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCATGACA GCGACGCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGTGCCG GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTGCGCGCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCGCTCTGA
1851 AGCCGAGCTG TGGGACGCGC CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCACGAAT TGAACCGTCA GCGCGCGAAG CAGGAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCCG
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTC
2251 GTCGGCTCAA GCCGCCGAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACC
2451 GCAGGTCGCC GCCCGCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGPELV
51 LDGSAKLLSV KINGVAADYV LEGETLTIA DVPSEFTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHQP
351 EDAGPTAHVP RPARYEEMNN FYTMTVYERK AEVVRMYHTL LGEFGQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMIPVK IGLLNCNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELPKHEKL LAAVEKVID
601 DLLDNAFKAL LLGVPSAEAL WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAK QENQSYEYSP EAAGWRTLRLN VCRAFLVLRAD PAHIETVAEK
701 YAEMAQNMTM EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QVQTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRA
851 QEGLSKDVG EIVGKILD*

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a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGPELV LDGSAKLLSV					
m665-1	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGPELV LDGSAKLLSV					
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGGRNVKIEFYTTTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YDLDFIMVAVGDFNMGAMENKGLNIFNTKFLADSRATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTPPTPDMDKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLLLAHDSDAFTRWEAAQTL YRRAVAANLAALSDGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLLGVPSEAE LWDGAENIDPLRYHQAREALLDILAVRFLPKWHELNROAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTL RNVCFVLRADPAHIETVAEKYAEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

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          790      800      810      820      830      840
          850      860
a665-1.pep  VKQALQRIHQEGLSKDVGEIVGKILD
|||||
m665-1      VKQALQRIHQEGLSKDVGEIVGKILD
          850      860

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1  ATGCTTTGTA TGAATTATCA ATCAAACCTCA GCGAAGGAG TGCTTGTAGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAC AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1  MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GCGAAGGAG TGCTTGTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAT AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

```

          10      20      30      40      50      60
m666.pep  MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g666      MLCMNYQSNSGEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTHSAVIAGADAHTPE
          10      20      30      40      50      60
          70      80      90     100     110     120
m666.pep  HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSAAADAMVAVQTTL SLVEPQSSGL

```

a666.seq

1	ATGCCTTGTA	TGAATCATCA	ATCAAACCTCA	GGCGAAGGAG	TGCTTGTTGGC
51	TAAAACATAT	TTATTGACTG	CATTGATAAT	GTCTATGACA	ATCTCTGGAT
101	GTCAAGTCAT	CCATGCCAAAT	CAAGGTAAGG	TTAATACTCA	TTCTGCTGTC
151	ATCACAGGTG	CAGACGCTCA	CAGCGCTGAA	CATGCAACGG	GACTGACCGA
201	ACAAAAGCAG	GTGATTGCAA	GTGATTTTAT	GGTAGCGTCA	GCCAATCCAT
251	TAGCAACACA	AGCTGGCTAT	GATATCTTAA	AGCAAGGCGG	TAGCGCTGCA
301	GATGCGATGG	TGGCGGTGCA	GACGACACTA	AGCTTGGTAG	AGCCACAGTC
351	GTCAGGCTTG	GGCGGTGGTG	CATTTGTGTT	GTATTGGGGAT	AATACCGCCA
401	AAACATTGAC	CACATTGAT	GGCGCTGAGA	CCGACCCGAT	GCGTGCGACG
451	CCGGAATTAT	TTTTGGATAA	AGATGGTCAA	CCATTGAAAT	TATGGAAGC
501	GGTGGTCGTG	GTCGCTCGGT	GGGTACGCCT	GCTATCCCTA	AACTGA

a666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	ISGQVIHAN	QGVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGSAA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLDKDGQ	PLKFEAVVVV	VARVRLLSL	N*	

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHTSA	VITGADAHTPE
a666		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHTSA	VITGADAHTPE
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQ	KQVIASDFM	VASANPLAT	QAGYDILK	QGGSAADAM	VAVQTTL
a666		HATGLTEQ	KQVIASDFM	VASANPLAT	QAGYDILK	QGGSAADAM	VAVQTTL
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLY	WDNTAKTL	TTFDGRET	APMRATPE	FLDKDGQ	PLKFMEAV
a666		GGGAFVLY	WDNTAKTL	TTFDGRET	APMRATPE	FLDKDGQ	PLKFMEAV
		130	140	150	160	170	180
m666.pep		NX					
a666		NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1  atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgctgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAttgcg
151 GAtttccttc agcgtgcccc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtcG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCAAttg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GCGTGTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACC GCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCTG TCGTCATCCG GCAGGGAAGA CCGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCgcCT
801 ATtgTgtcat TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1  MRFVFC LGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGAV MQYGVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNVLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEFVIRGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRL LCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1  ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACC GCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCGAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1  MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHPIAR GVDVYQGAV MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10          20          30          40          50          60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
          | | : : | | : : | | : : | | : : | | : : | | : : | | : :

```


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```

g667      MRFVFC LGGEIVSDPCDFHLVFVRVESAADQTETQIHQIRIHGIGFAIIADFLQARVER
           10      20      30      40      50      60
           70      80      90      100     110     120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
g667      FPHFAAVHTQLARKAAQFRHIVQRHIRPRLVKREQIHQIAVALVITADVVPLEIAAAVE
           70      80      90      100     110     120
           130     140     150     160     170     180
m667.pep  IAVAHIP IARGVDAVYQGAVMQYGOIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
g667      IAVARIPIARGVDAVYQGAVMQYGOVETAAPADQLRRMFFNQFEKLGNDFFAIVHLAD
           130     140     150     160     170     180
           190     200     210     220
m667.pep  GADMYFILPPTHAARNRHNLMKMLHKIAARLSTAFVLGNQHHL
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
g667      GADMNVLVPPAHTAGNRHNLMEVVLHKIAAGLCAAFLLREQHHFVIRQGRROVIQRTDTL
           190     200     210     220     230     240
g667      HIGYGFNIESQNRHIGSTLHSKTDLRLLLCHX
           250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2181>:

```

a667.seq
1  ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTCCATTTC GTATTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG CGTGGAACGC CTCCACACCC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTGTAGCA GCGAACGTA ATGCAGAACC GGCAGGTCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAAA CAGCACCAC TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TAAAA.CAG ACTTGCGCCT
801 ATTGTGTCAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2182; ORF 667.a>:

```

a667.pep
1  MRFVFC LGGE IVSDPLDFHF VFVCVESAAD QTETQIHQIG IYRIGFAIIA
51  DFLQPARVER LPHLAAVHTQ LARKTAQFRH IVQRHIRPRL VKREQIHQIA
101 MTLVVAADV VPLEIAAAVE IAVAHIP IAR GVDV*QRTV MONRQVETAA
151 VPTDQLRRMF FNQLEKFGDN HFLAVIHLAD CTDMDFILPP THAARNRHNL
201 MKMMLHKIPT RLSTAFLLGK QHHFIVGORG RQVIQRTDTL HIGYGFNIES
251 QNRGHDSTLY LKXDLRLLLCH *

```

m667/a667 79.0% identity in 224 aa overlap

```

           10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPFDHFVVRVRIQPAADQTETQVHQSVCVRVGFIAIADFLQPARMEC
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
a667      MRFVFC LGGEIVSDPLDFHFVFVCVESAADQTETQIHQIGIYRIGFAIIADFLQPARVER
           10      20      30      40      50      60
           70      80      90      100     110     120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
a667      LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLVVAADVVPLEIAAAVE

```

	70	80	90	100	110	120
m667.pep	130	140	150	160	170	180
	IAVAHIPIARGVDAVYQGAVM	QYGGIETAAVPTDQLRR	MFFNQFEKFSNDHFLAVI	HLAD		
a667						
	IAVAHIPIARGVDAVXQRTVM	QNRQVETAAVPTDQLRR	MFFNQLEKFGDNHFLAVI	HLAD		
	130	140	150	160	170	180
m667.pep	190	200	210	220		
	GADMYFILPPTHAARNRHNLM	KMMLHKIAARLSTAFVLGN	QHHL			
a667	:					
	CTDMDFILPPTHAARNRHNLM	KMMLHKIPTRLSTAFLLG	KQHHFIVGQRGRQVIQRT	DTL		
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYL	KXDLRLLCHX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

g669.seq

1	ATGCGCCGCA	TCGTTAAAAA	ACACCAGCCC	GTAAACGCGC	CACATATCGT
51	TTTGGAAATT	CGGATAATGA	AACTGCATCG	CGCGTTTGTC	TTCCTTGGGC
101	GGAAACGTC	CACATCAT	GACCGCAGCC	TTCGGCGTCA	ACACGGGATC
151	GAAGGATGG	GTTTCGATT	CAAGCAGATT	TTCAGACACG	TTCAATCCTC
201	CAACAGGCA	AGCGGCAGAC	AGCCGGTTTG	CACCAAACCG	CCAAACACGG
251	CAAGCCTTCA	AACAGCATTA	TCACGCCCTG	CCGTTTTTCG	TTACAATGCC
301	GACATCAAAC	GGATACGTGA	A		

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

g669.pap
1 MRRIVKKHQP VNAPHIVLEI RIMKLRHAFV FLGRKRPHHH DRSLRRQHGI
51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```
m669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGCTCC CCATCATCAT GACACGAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAACTCCT
201 CAACAGGCAA AACCGGCAGC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTTCG TTACAATGCC
301 GACATCAAAC GGATACTGTA A
```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```
m669.pep
  1  MRRIKKHQP INAPHIVLEI RIMKLHRAV FLGRKRPHHH DSSLRRQHGI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQ TAL SRPAVFGYNA
101  DIKRIL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

```

      10      20      30      40      50      60
m669.pep  MRRIKKKHQPINAPHIVLEIRIMKLHRAVFVFLGRKRPHHHDSLLRRQHGIEGMGDFKQI
          |||:||||:|||||||||||||||||||||||||||||||||||||
g669      MRRIKKKHQPVNAPHIVLEIRIMKLHRAVFVFLGRKRPHHHDSLLRRQHGIEGMGDFKQI
      10      20      30      40      50      60
          70      80      90     100

```

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
  1  ATGCGCCGCA TCATTAATAA ACACCAGCCC GTAAACGCGC CACATATCGT
 51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101  GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151  GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201  CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251  CAAGCCTCA AACAGCATT TACGCCCCTG CCGTTTTCGG TTACAATGCC
301  GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
  1  MRRIKKHQP VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRQHGHI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTK PNTASLQTAL SRPAVFGYNA
101  DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAVFLGRKRPHHHDSLRRQHGIEGMGFDFKQI
              |||||:|||||
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGIEGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
  1  ATGACTTGTT GCAGGAAC TG CTTGGCGCGT TCGTGTTTCG GGTGTTGTA
 51  AAACGCTTCC GCGGTTTCG CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101  TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTTCGTG GGTACGCAC
151  ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201  GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251  CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301  CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351  GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTC GCATTTTGCC
401  CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451  GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
  1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
 51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101  PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151  G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
  1  ATGACCTGTT GCAGGAAC TG CTTGGCGCGT TCGTGTTTCG GGTGTTGTA
 51  AAACGCTTTC GCGGTTTCG CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101  TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTTCGTG GGTACGCAC
151  ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201  GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTTCGTCA AACAAACATTA

```

```

251  CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301  CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351  GCGTTCCAAA AGTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401  CCTAACCTT CATCGGTGCG AGGGAATGT TTTCCAACAC GGTGAGGTGC
451  GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101  PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151  G*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAK PRAIATRCCWPPESWEGKASFLCASPTRSK
              |||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||
g670           SSIAFFSACS AFCPLTFIGARVMLSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTAAA
 51  AAACGCTTCC GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101  TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTACGCAC
151  ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201  GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCTGCA AACAACTTA
251  CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301  CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351  GCGTTCCAAA AGTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401  CTTAACCTT CATCGGTGCG AGGGAATGT TTTCCAACAC GGTGAGGTGC
451  GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51  IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101  PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151  G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
             |||
a670         FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
             |||
a670         SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201 GCGGAGGTcg gcgaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGAGGCAAA
201 GCGGAGGTcG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR
             |
g671         MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL

```



```

a671.seq
1  ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CCGTGTGGCA AGCCCAAACC GACCGCCGAA ACTGCCCOGG
101 TCAGCAGCGA CGGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGTGA ACGATGCAAA
201 GGCATGTCTG GCGAAGGGTG CGGCAAAGAG TTTGGCGAAA AAAAAGGCCA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCAGCA TGCAGGCGGC GATGATGGCG GAGACAGGGA GGTCGGCCAA
351 GGGGAGGTTA TTCATTCTGT ACCTGACCGG CGATACCGTA TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

```
a671.ppe
1 MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51 EMNDRANANR RGWNDAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
```

```

                                10      20      30      40      50      60
m671.pep  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
          |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a671      MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
          10      20      30      40      50      60

                                70      80      90      100     110     120
m671.pep  RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL
          ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a671      RGWNDAKAMSAKGAAKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
          70      80      90      100     110     120

                                130     140     149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a671      FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          130     140

```

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCACGCGC	GCGCAGACGC	ATTGGGACTG	GTTTTTTACC
101	CCCAAAGCCC	CCGCGCTATC	GACATCATT	AAGCACAAA	AATCGCCGCC
151	GCACTGCCGC	CGTTTGTCTAG	CGTTGTCTGCC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	GCCGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CCGCCCTTAT
301	ATTAAGCCCA	TTCTGTGTTCA	GACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	GCGCTTCCCC	AACGCTCAGG	CAGTCTGTT	CGATGCCTAT	CACCCCTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	Ggacgtgttt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCCTG	AAAACGTCGG
501	CGAAGCCGTC	CGCATCACCG	GAGCGGAAGC	GGTCGACGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGCCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTTATC
601	GCAACCGCCA	ACCGCTATC	CCGTTAA		

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAAKVAAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICG	ITTPEDAAAA	AAGADAVGL	VFFQSSRAV	DIARAKKITA	ALPPFVSVVA
g672	10	20	30	40	50	60
	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYQSPRAI	DIIKAQKIAA	ALPPFVSVVA
m672.pep	70	80	90	100	110	120
	LFVNESAQN	IRRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRF
g672	70	80	90	100	110	120
	LFVNESAQN	IRRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRF
m672.pep	130	140	150	160	170	180
	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	130	140	150	160	170	180
	NAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
m672.pep	190	200	209			
	SGGVEASKGK	KDAKVAAFI	ATANRLSRX			
g672	190	200				
	SGGVEASKGK	KDKPAKVAAFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCGCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTGTC CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACCGCCA ACCGCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITPEDALYA AHAGADALGL VFYQSPRAV DIIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

              10      20      30      40      50      60
m672.pep      MRKIRTKICGITTPEDAAAAAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              10      20      30      40      50      60
m672.pep      LFNESAQNIRRLAEVPIHIIQFHGDEDDAFRCRQFHRPYIKAIRVQTASDIRNAADRFP
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              70      80      90      100     110     120
m672.pep      LFNESAQNIRRLAEVPIHIIQFHGDEDDAFRCRQFHRPYIKAIRVQTASDIRNAADRFP
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              70      80      90      100     110     120
m672.pep      DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              130     140     150     160     170     180
m672.pep      DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              130     140     150     160     170     180
m672.pep      SGGVEASKGKKDAAKVAEFIATANRLSRX
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              190     200     209
m672.pep      SGGVEASKGKKDPAKVAEFIATANRLSRX
a672           |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGTAAG CAACTGCCCA AGCACACGCC GGTCATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCCGAAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTCCGT GAAAACTCT TCCGCTATTT

```



```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
  1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
 51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

m673.pep      10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
|||||
g673          10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
|||||

m673.pep      70      80      90     100     110     120
YTDDTAQFVFVDTPGFQTDH RNALNDRNLQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
|||||

```

```

g673      YTDDTAQFVFDTPGFQTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGCGC
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCAGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGCTTTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDTK VFLKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFGTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFGTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGGLNR					
a673	KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

g674.seq

1	ATGAAAACAG	CCCGCCGCGG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAAATTGCT	AAAAACATCC
101	GCGAAATGTC	CGACTTTGCC	AAAGCGGACG	AAGAATTGTT	CAACAAACTC
151	TTCTTCGGCA	CACAAACCAA	TGCAGCGGAC	TACATCCAAA	AAATCCGCCC
201	GCTGCTCGAC	AGGGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTTT
251	TGCTGACCGC	CTGCCACGAG	CTTTCCGCTA	TGCCCGAAAC	GCCCTACCCC
301	GTCATTATCA	ACGAAGCCAT	CGAAGTTACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCAAATCC
401	GCCCAGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

g674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMSDFA	KADEELFNKL
51	FFGTQTNAAD	YIQKIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGKH	FVNGILDKLA	AQIRPDEPKR	R*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

m674.seq

1	ATGAAAACAG	CCCGCCGCGG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAAATTGCT	AAAAACATCC
101	GCGAAATGTC	CGACTTTGCC	AAGCGAGACG	AAGAATTGTT	CAACAAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TATATCCGAC	AAATCCGCCC
201	GCTACTTGAC	AGGGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTTT
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCGAAAC	GCCCTACCCC
301	GTCATTATCA	ACGAAGCCAT	CGAAGTTACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCAAATCC
401	GCCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

m674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMSDFA	KADEELFNKL
---	------------	------------	------------	------------	------------

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAACAG	CCGCGCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CGCGCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacggtc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEM	LKVCCRTLQELGVADENITVATVPGALEIP				
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAACAA GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV

```

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC	CRTLQELGVADENITVATVPGALEIP				
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC	CRTLQELGVADENITVATVPGALEIP				
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE	LSNESGAGVSRVALDYNIP	IANAVLT	TEN		
a675	IALMNFASSEKFDALIAIGVVIRGETYHFE	LSNESGAGVSRVALDYNIP	IANAVLT	TEN		
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVA	VECANLVNLLLEE	QFEDEEX			
a675	DAQAIERIEEKASDAKVA	VECANLVNLLLEE	QFEDEEX			
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
51 ggAAACGGTG CGCTTGCGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCGGGCGT
151 GTTCAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACGCGCCA
201 ACGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGACG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTCGCGCCG AAAAATACTT GGTGGTTCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTTCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GGCCTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CCGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
1 MPQILVRIFL IRYSEFIWETV RLCRFRHRHS SVDFDVDRK DFNFLTAFR
51 VQNHFAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
101 GRAEYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGGCGT
151 GTTCAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
301 CGTCGCGCCG AAAAACACTT GGTGGTTCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTTCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GGCCTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CCGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
1 MPQILVRIFL IRYSEFIWETA RLCRFRHRHS SVDFDVDRK DFNFLTPFR

51 VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDKDFNFLTFFRRVQNHFAFAR					
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDKDFNFLTAFRRVQNHFAFAR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG					
	:					
g677	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKYLVRFAQFGIDDDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL					
g677	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL					
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCCTCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAACC	ACTTCGTGCG	CTTCACGCGC	TTTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTTCGCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAACACTT	GGTCGGTTCG	TCGCCGCAAT	TCGGGATCAA
351	CGACGACGGC	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTTCG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCCC	AGTTGACGAT	TTGGACGATT	TCGGGCGGTT
501	CTTTATTAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTTTGGT	TTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVFDK	DFNFLTFFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQTD
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVAVFAA
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDKDFNFLTFFRRVQNHFAFAR					
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDKDFNFLTFFRRVXNHFAFTR					
	10	20	30	40	50	60
	70	80	90	100	110	120


```

m677.pep      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
a677          FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
a677          GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
a677          PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcggCCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TGCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTt TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCCTcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TFCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcctGT TTGCATTGGC
201 TCTGTGCTTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTt TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

```

      10      20      30      40      50      60
m678.pep  MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g678      MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m678.pep  PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g678      PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          70      80      90      100     110     120

      130     140     150     160
m678.pep  VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g678      IMLASKTDLPDTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGC CGCGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCG CCAAACTCTT TGCCGACCCC
151 TTCGCCGACA TCGCCTTTCG ATCGTTCCAA CCGCGCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51 FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLTGT AVSAVGLGFA
101 NRILGGVFGA LKGILIIITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

```

      10      20      30      40      50      60
m678.pep  MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a678      MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m678.pep  PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a678      PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILIIITLL
          70      80      90      100     110     120

      130     140     150     160
m678.pep  VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a678      VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51 GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTTCGA
101 GCCTGCTTGT TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGTTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GGCACGACT ATTTTCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGCA
101 GCCGCTTTT TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTC AATGCAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGAGTTG
301 GCGTTGGTGG TGTTCGCGC GGCAGCTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATAAGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCACGACG ATTTTCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPKN TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680       MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRF*MXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680       TLCLVLQKTITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAELVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

```

g680      |||||::|||:||||:|||||
          ASLRIGAEKVAEKSRVWRWRSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
           130       140       150       160       170       180

           190       200       210       220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPPNKT VWRSGRFLMX
          |||||::|||:||||:|||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVC RSGRFLMX
           190       200       210       220

```

a680.seq

1	ATGACGAAGG	GCAGTTCGGC	AATATCCAGC	CCCCGCGCGG	CGATATCGGT
51	GGCGACGAGG	ACGCGCAGGT	TGCCGTCTTT	GAAGGCGTTG	AGTGTTCGA
101	GCCGGCTTTG	TTGGGAACGG	TCGCCGTGTA	TCGCCTGTGC	GGACAGGTTG
151	CGGCGCACCA	GTTTCGCGCT	TACGCGGTGC	ACGCTTTGTT	TGGTTTTGCA
201	GAACACGATG	ACCTGTTTCA	TATGCAAAAT	GACAATCAGC	CGTTCGAGCA
251	GGTTGCGCTT	CTGAATGGTA	TCGACGGCGA	TGATGTGCTG	CTCGACGTTG
301	GCGTTGGTGG	TGTTCTGCGC	GGCGACTTCG	ACGGTTTCGG	GCGCGTTCAT
351	GAAGTCTTGC	GCCAGTTTGC	GTATCGGGGC	GGAGAAGTTG	GCGGAAAAGA
401	GACGGGTTTG	GCGTTGGCGG	GGCAGCATCT	GCATGATTTT	GCGGATGTGC
451	TCGATAAAAC	CCATATCCAG	CATACGGTCG	GCTTCGTTCA	AAACGACGAT
501	FTCGACTTTG	TTCAAATGGA	TGTTTTTCTG	TTTCACGTGG	TCGAGCAGCC
551	GTCCGACGGT	GCGCAGCAG	ATTTCGCAGC	CGGCACGCAG	GTCGGCGGTC
601	TGTTTTGTCCA	TATTCATACC	GCCGAACAAG	ACGGTGTGGC	GCAGCGGCAG
651	GTTTTGTATG	TAG			

a680.pep

1	MTKGSSA	ISS	PRAAISV	TRRLPSL	KAL	SVSSRLC	WER	SPCIACAD	RRL
51	RRTSSRV	TRS	TLCLVLQ	NTM	TWFICKS	TIS	RSSRLRF	*MV	STAMMCC
101	ALVVSCA	ATS	TVSGAFM	KSK	ASLRIGA	EKV	AEKSRV	VWRWR	GSICMIL
151	SIKPISS	IRS	ASSKTTI	STL	FKWMFFC	FTW	SSSRPT	VATT	ISQPARR
201	CLSIPIPP	NK	TVVRSGR	FLM	*				

		10	20	30	40	50	60
m680.pep		MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
		: :					
a680		MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
		10	20	30	40	50	60
		70	80	90	100	110	120
m680.pep		TLCLVLQNTMTWFICKSTISRSSLRFXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC					
a680		TLCLVLQNTMTWFICKSTISRSSLRFXMVSTAMMCCSTLALVVSCAATSTVSGAFMKSC					
		70	80	90	100	110	120
		130	140	150	160	170	180
m680.pep		ASLRIGAELKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					
a680		ASLRIGAELKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					
		130	140	150	160	170	180
		190	200	210	220		
m680.pep		SSSRPTVATTISQPARRSAVCLSFIFPPNKTVWRSGRFLMX					
a680		SSSRPTVATTISQPARRSAVCLSFIFPPNKTVWRSGRFLMX					
		190	200	210	220		

g681.seq
1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTTCGG AAGAGGCAAA
51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCqacqg

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GCGGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GGTGCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTTCCGCGT TGTGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCCCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

g681.pep

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGLEEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VFVGVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

m681.seq

```

1  ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 TGGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

m681.pep

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||
g681      MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

1092

```

              70      80      90      100      110      120
m681.pep      KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGDGLECAVFGKLPCAA
              |||||
g681          KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGNGLCAVFGKLPRAA
              70      80      90      100      110      120

              130      140      150      160      170      180
m681.pep      FGLGEQCGGFRVGFVDGVEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP
              |||||
g681          FGLGKQCGGFRVGFVDGVEADDAEVVGVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP
              130      140      150      160      170      180

              190      200      210      220      230      239
m681.pep      VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVCAPFAA
              |||||
g681          VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVCAPFAA
              190      200      210      220      230      240

              240      250      260
m681.pep      LRCFCIFGVWKRIRAVFCGRRX
              |||||
g681          LRCFCIFGVWKRIRAVFCGRRX
              250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCGTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTGCTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGAAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1   IITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFGVLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

```

              10      20      30      40      50      60
m681.pep      MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
              :
a681          IITPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
              10      20      30      40      50      60

              70      80      90      100      110      120
m681.pep      KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGDGLECAVFGKLPCAA
              |||||
a681          KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVGDGLECAVFCQFPRAA
              70      80      90      100      110      120

```

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
a681	FRLGEQCGGFRVGFVDIGEADDAEVVRVVG FVGLVAAEETPAAVVFKNGGFAVEEADGL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGXKLTDFTTIRALSADGGGLVVQCAPFAAL					
a681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTXGGKLADFTTILALSADGGGLVVQCAPFAAL					
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIRAVFCGRRX					
a681	RCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGTTTCC AACTGACCGA
301 CCCATTCCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. ..EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:|||||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDWIoTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          ||||| |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEPDWIoTAFCMAGFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      YPTRSLPKSKKAYGX
          120     130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```

a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
 51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101  TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151  ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201  ATAT.....
251  .....TATA TTCGTTTCC AACTGACCGA
301  CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTGCG CACGAACGGG
351  TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401  GA

```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```

a682.pep
  1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
 51  ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101  PILTRPTGVV RISPTGFRY PTRSLPKSKK AYG*

m682/a682  80.6% identity in 129 aa overlap

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWIoTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
          ||||| |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
          70      80      90      100

      130
m682.pep  LPKSKKAYGX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      LPKSKKAYGX
          110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
  1  ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTACT
 51  CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101  AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151  GACAGTGTGA GAAAAACGGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201  TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251  CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301  AGTTTCGTAC AGTTATTGTA TACAAAAAAC ACGGAAATT CCACACAAA
351  CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA

```


401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTAAACAAG AACGTTTTGC CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
g683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
g683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTTACCAAT CTAAACAAG AACGTTTTGC CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

```

      10      20      30      40      50      60
m683.pep  MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||||
a683      MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||||
      70      80      90      100     110     120
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
          |||||
a683      IFXDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
          |||||
      70      80      90      100     110     120

      130     140
m683.pep  SSLRPMISLSGLTEKQYETVCGKKLX
          |||||
a683      SSLRPMISLSGLTEKQYETVCGKKLX
          |||||
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

```

g684.seq
1  ATGCGCCTTT TCCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51 TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAC CTTTGTTCCT
301 GCCTCAGGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

```

g684.pep
1  MRLFPIAAAL TLAACGTVQS TOYFVLPDSR YIRPATQGGG TAVEVRLAEP
51 LKRGGGLVYQT DPYRINTAQN HVWADTLDDM LEAALSNAFN RLDSTRTFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTALE QGLKQAAQQM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

```

m684.seq
1  ATGCGCCTTT TCCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51 TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCAGGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

```

m684.pep
1  MRLFPIAAAL SLAACGTVQS TOYFVLPDSR YIRPATQGGG TAVEVRLAEP
51 LKRGGGLVYQT DPYRLNTAQN HVWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTKEW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```

151 GYAAMTAALE QGLKQAAQOM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPFIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT					
g684	MRLFPFIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT					
	10	20	30	40	50	60
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
g684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
g684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPFIAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGGE	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSRGSTKWT	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQOM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPFIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT					
a684	MRLFPFIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT					
	10	20	30	40	50	60
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
a684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
a684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

m684.pép YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
|||||
a684 YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
130 140 150 160 170

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

g685.seq
1 TTGTTTTGCC GTATCGGGAA TTTTGCCTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCTT GCCGGCCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAAT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCGTCGCCA CGCTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgtcg ccgtgtAcga CtggGCGGCG
301 TtggATACGC TGACCGAGCC GGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTGC AGCCTGCATT TGACAAGCGG GCAACCGTGG
401 GGACGCTGTT TGAGCCCGAT TCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCTATTA CCGCGGGGCC GGGTGCAGAA GCGTATGAAC AGTTGGCGAA
501 AAACCGGACC ACCATAGATT TGACGGTGGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTTCG CCCAAAGCG
651 CGAAGCGGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GGCGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CGGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >:

g685.pép
1 LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51 CSPEPAAEKT VSAASQAAS PVATLTVPTA RGDVVPKPN ERVAVYDWAA
101 LDTLLEPGVN VGATTAPVRV DYLPAPFKA ATVGTLFEPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNNG IRTSGEKOME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AAIGQEGPAA
301 VEVLDNAIVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

m685.seq
1 TTGTTTTGCC GTATCGGGAA TTTTGCCTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCTT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAAT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCCGGCCGG TGCCTGTGGA
351 TTATTTGCAG CCGTCAATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCTATTAC
451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCGGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTATCATCG
851 ACCGTACCGC CGCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGGAAGCGCA AGCAAATCAT
951 CGTCATGCTT GCGCGGAAT ACATTGTGCG GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTAATAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pép

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
              |||||
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              |||||
g685           VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep      DYLPAPFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
              |||||
g685           DYLPAPFDKAATVGTLEFPDCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRGVLVSVTGNKVSAGF
              |||||
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGGKRGVLVSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
              |||||
g685           TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep      VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX
              |||||
g685           VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGCCT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCCTGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGCGCGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GGGCGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCAGAAAAGC
551 AGATGGAGAG CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCACTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCTTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 CCGCGCGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKOMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSFAFGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

m685.pep	10	20	30	40	50	60
a685	10	20	30	40	50	60
m685.pep	70	80	90	100	110	120
a685	70	80	90	100	110	120
m685.pep	130	140	150	160	170	180
a685	130	140	150	160	170	180
m685.pep	190	200	210	220	230	240
a685	190	200	210	220	230	240
m685.pep	250	260	270	280	290	300
a685	250	260	270	280	290	300
m685.pep	310	320	330	340	350	
a685	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

g686.seq (partial)

```

1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTGTGCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
 101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
 151 GGCTTCGGCG GCATTGCCCC ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
 201 CGCGTTTGAA TCCGTGCGCT ACTCCTTGCG TCAGCATACT ACCGGCATTG
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
 401 TCGCGGGGAT GGTGTTCGTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
 451 TCCGTCAACG GGACTACCGG CTTTCATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
 51 GFGGIARVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGMVFV SVPMDAVKAK
 151 SVNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGGSEGGSGAXX	10	20	30	40	50
				40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		70	80	90	100	110
		80	90	100	110	120
g686.pep		100	110	120	130	
		GIAAALWPVIAVGMVFVSVPMDAVKAESVNGTTGFVRIGMX				
m686		130	140	150	160	
		GIAAALWPVIAVGMVFVSVPMDAVKAESVNGTTGFVRIGMX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
 51 TGAAAGCTTC GGCAGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
 151 ATTGTGGAAG CGGTCGACAA GCCGTGTGCC GGTGCTGCGG TTGTGCGTCA
 201 GGTGAGGCG GATATTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51 IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep    LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDDICSAVEGFGGIARSVQLG
a686                |||||:|||||:|||||:|||||:|||||:|||||
                NFSCRADDVFNDDICSAVESFGGIARSVQLG
                        10      20      30

              70      80      90      100     110     120
m686.pep    AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686                |||||:|||||:|||||:|||||:|||||:|||||
                AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                        40      50      60      70      80      90

              130     140     150     160
m686.pep    GIAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
a686                |||||:|||||:|||||:|||||:|||||:|||||
                GIAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
                        100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GGCCTTGCCG CCCTGTTCCG
51  CCTTGCCCGC TCGGACAGCA AAGTCCAAAC CAGCGTCCCC GCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGCG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTTCG GCTATTTTTC TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCACGCct
351 cGCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAA ACcgccctTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTGCGC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGCG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687 >:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGO
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWVQKE MLPLARLAAA VDMAAESKD VANSHIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGGKVL AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGCGCCTG
101 CGGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACCGTCTTTC CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACGCC TTTGACGGCA AAAAAGTCCT

```



```

501 TGCCGCCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

m687/g687 97.0% identity in 234 aa overlap

```

              10      20      30      40      50
m687.pep  MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              10      20      30      40      50      60

              60      70      80      90      100     110
m687.pep  QQQAGKVEVLEFFGYFCPHCAHLEPVL SKHAKSFKDDMYL RTEHVWVQKEMLT LARLAAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      QQQAGKVEVLEFFGYFCPHCARLEPVL SKHAKSFKDDMYL RTEHVWVQKEMLPLARLAAA
              70      80      90      100     110     120

              120     130     140     150     160     170
m687.pep  VDMAAADSKDVANSHIFDAMVNQKIKLQNPV LKKWLGEQTAFDGKKVLAAYESPESQAR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      VDMAAAESKDVANSHIFDAMVNQKIKLQEPV LKKWLGEQTAFDGKKVLAAYESPESQAR
              130     140     150     160     170     180

              180     190     200     210     220     230
m687.pep  ADKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      AGKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAAGCGT CCCC GCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N. meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

m687.pep	10	20	30	40	50	60
	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIPQQ					
a687	10	20	30	40	50	60
	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIPQQ					
m687.pep	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLKSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
a687	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLKSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
m687.pep	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNEPVLKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNEPVLKWLGEQTAFDGKKVLAAYESPESQARAD					
m687.pep	190	200	210	220	230	
	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	190	200	210	220	230	
	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGTCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAEAL	RAKQNAQKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGTCACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCCTGTGTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSTRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

m688/g688 90.6% identity in 138 aa overlap

```

      10      20      30      40      50      60
m688.pep  VLHYPFRFAQKGISVNKTLILALSALLGLAACSAERVSFLFPSYKLIKIIQGNELEPRVAA
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688       VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVSRVSLFPSYKLIKIIQGNELEPRVAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m688.pep  LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTIVYFENGVLVRTEG
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688       LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTIVYFENGVLVRTEG
          70      80      90     100     110     120

      130     140
m688.pep  DVLQNAAEALKDRQNTDKPX
          ||||| ||| :|||
g688       DALQNAAEALRAKQADKQX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```

a688.seq
1  GTGTACTACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAT CATAACAGGC
151 AACGAACCTG AACCTCGCGC CGTCGCCTCC CTCCGCCCGG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```

a688.pep
1  VLHYPFRFAQ KGISVNKTLI LALSALLGLA ACSVERVSFL FPSYKLIKIIQ
51 NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLTIVYF ENGVLVRTEG NALQNAAEAL RVKQADKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

```

      10      20      30      40      50      60
m688.pep  VLHYPFRFAQKGISVNKTLILALSALLGLAACSAERVSFLFPSYKLIKIIQGNELEPRVAA
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688       VLHYPFRFAQKGISVNKTLILALSALLGLAACSVSRVSLFPSYKLIKIIQGNELEPRVAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m688.pep  LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTIVYFENGVLVRTEG
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688       LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKDRSNLTIVYFENGVLVRTEG
          70      80      90     100     110     120

      130     140
m688.pep  DVLQNAAEALKDRQNTDKPX
          ||||| ||| :|||
a688       NALQNAAEALRVKQADKQX
          130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```
1 ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51 GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCGCGA
101 TTCCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCGAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGGCGAG GCATGGCTGT
351 AGTCATCGTc ggtgcatgg tgcgcgatTA TTATTCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
451 GCACCCATGG TCGGCGCATT GTTGCAGGGA TTGGGCGGAT GGCGGGCGAT
501 TTTTCGTTTTT ttggcGgcat ATTTCGCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTGCCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTCAGG CATTACAGCT CGGTTCGATG TTCGCCCTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGGTGTTCG ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAAACCCG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTGCTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTCC GTCGCTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCTG
1051 GGTGTTATTC GGTCTTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGCGGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAAA GCGAATACTT
```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```
1 ..SPPLPPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51 SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLNLRVAVQA FGAGMAVIV GAMVRDYYSR RKAQMFLAI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPV LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLETSSFV YRQLYHVTPH
251 RYAVVFALNI ITMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301 AVLFFGLPEF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```
1 TTGTAAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51 GTTGCCGCCT GTTGTGCGG GTGTGTTAAA ATTTCCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCGGACG AGAATTTATG
151 CTTCTGCCC ATTATCCTGA AATGAGCGAA AACTGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTGTGTTAT GTTCGGCAGC GCCTTCGGAC AGGTGGTCCG
351 CGGTTTCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGCACGAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGTTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTCAG CTTGCGTTCT ATGTTTCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGTTACGCTT
901 CATCAATACG CTTGGGCGTT TGCACCAAC ATCATCAGC TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTT GTCCCAACTC
1051 GCCGCGGTGC TGTTTTTCGG GTTGCCCGCG TTTGGCTGCT TGGTCCGCTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGACGG
1151 CGTGTGTTAT GTCCTATTTT AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGGC TCTGCTCGCA TCGTCCGTGG
```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep

```

1  LLIHVIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPAV LTGLIVYCLA VAAIVFVSSA
151 EQLNLNRVVO AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH POSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSDAY					
g689						
				SPPLPPMSGKLMMAVLMVALMPFSIDAY		
				10	20	30
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLNLRAVQAFGAGMAVVIVGAMVRDYYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFRKRV					
g689	APMVGALLQGLGGWRAIFVFLAAYSPVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFRKRV					
	160	170	180	190	200	210
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFSGVTQGLVGAD					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMFSGVTQGLVGAD					
	280	290	300	310	320	330
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360	370	380	
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

a689.seq

```

1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTGTGCGCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCCA AATGGCGCAG TCGTGAACG CCGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGTCTA CTGCCCTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCGGTG CGGGCATGAC
501 TGTGGTCATC GTCCGCGCAA TGGTGCGCGA TTATTATTC GGACGCAAAG
551 CCGCCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTGGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTTCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCGC
801 GATGGGTAT CTGTTTTTTC AGGCATTAG CTTCGGTTTC ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCACCTCAAC ATCATCACGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CCGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTCG TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTT AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGCGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

a689.pep

```

1   LLIHIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYSY GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIIV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYHVTP
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA VGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

m689.pep	10	20	30	40	50	60
a689	10	20	30	40	50	60
m689.pep	70	80	90	100	110	120
a689	70	80	90	100	110	120
m689.pep	130	140	150	160	170	180
a689	130	140	150	160	170	180
m689.pep	190	200	210	220	230	240
a689	190	200	210	220	230	240

```

a689      |||||
          GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSILVLLGLVQYFLPKP
          190      200      210      220      230      240

m689.pep      250      260      270      280      290      300
          AVGGKIGRDVFLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
a689      |||||
          AVGGKIGRDVFLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVTP
          250      260      270      280      290      300

m689.pep      310      320      330      340      350      360
          HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVFFGLPP
a689      |||||
          HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVFFGLPP
          310      320      330      340      350      360

m689.pep      370      380      390      400      410      420
          FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLG V FQSLIGAGVGM AATFLH
a689      |||||
          FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLG V FQSLIGAGVGM AATFLH
          370      380      390      400      410      420

m689.pep      430      440      450      460
          DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
a689      |||||
          DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1   ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAAC CGATTTGCAA
151 CCGGCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCTGC ACCCCGCGCG CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGGCGGCT ATGACAACAT
351 ACAGCGGCTG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAA CCGCACCATC
451 AGccgGCAGG CACAAATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGC GGaCAAGGCG
551 AGGAACCGAA ACGGCACGCT TATTTGAAAG TTTCGGCAAC ATCtgCctat
601 TTgaaccggc ACAaCaacGG ACTTggcgGC AATTTCaAT ACATCGGCCA
651 ATTGCCCCGG TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCaaTCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1   MKNKTSSLPL WLAAIMLAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHOKIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEFPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq..

```

1   ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTG CAT
101 CCGCTGCTTC GTCTCCGCG TCATCAGCTC CTTCCCAAAC CGATTTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCACGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACC CGC GGaCAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

m690.pep

```

1 MKNKTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQOIAEHI DSDCLFALSH
101 HELETRFGLP DGYDNIQRL LFPDIRPEDP DYHQIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEKTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHEMLE NQSLFRLSNR ERNPKPFLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

m690/g690 89.3% identity in 408 aa overlap

```

m690.pep      10      20      30      40      50      60
MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPSQTDLQPTASAPDNVK
g690          10      20      30      40      50      60
MKNKTSSLLPLWLAAILAARSPSKEDKTKENGASAASSSASSQTDLPAAAPDNVK

m690.pep      70      80      90      100     110     120
QAESAPPSNCTSLHPATGIDDLMQOIAEHI DSDCLFALSHHELETRFGLPDGGYDNIQRL
g690          70      80      90      100     110     120
QAESAPLXNCTGLHPAAGIGDLIQOIAEHI DSDCLFALSHHELETRFGLPDGGYDNIQRL

m690.pep     130     140     150     160     170     180
LFPDIRPEDPDYHQIILAI EDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
g690         130     140     150     160     170     180
LFPDIRPEDPDYHQIMLAIEDLRYGRTISRQAQDAIMEQERRLREATLMLTQGSQKTR

m690.pep     190     200     210     220     230     240
GQGEPEKTRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHEMLENQSLFRLSNR
g690         190     200     210     220     230     240
GQGEPEKRRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLMHGEMLNQSLFRLSNR

m690.pep     250     260     270     279
ERNPKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
g690         250     260     270
ERNPKPFLDIHFDENGKITRIVVYEKNIY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

a690.seq

```

1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51 GACCGCGTGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCGCGCTC GTCCACGGCA TCCGCGCGCT CGTCTTCCGC GCCCCAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAATTGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCCG CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCACGATCA GCCGGCAGG ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCAGCGGTT ATTTTGAAAT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAA

```


1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFFDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFOYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50
m690.pep	MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLOPTASAPD			
a690	MKNKTSSLLLWLAAMMLTACSPSKEDKTENGASAASSTASAASSAPQTDLQPAASAPD				
	10	20	30	40	50
	60	70	80	90	100
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI				
	70	80	90	100	110
	120	130	140	150	160
m690.pep	QRLFFDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQNALMEQERRLEATLLLIQGSQ				
a690	QRLFFDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQDALMEQERRLEATLLLIQGSQ				
	130	140	150	160	170
	180	190	200	210	220
m690.pep	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFOYISQLPGYLKIHGEMLLENQSLFRL				
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFOYIGQLPGYLKIHGEMLLENQSLFRL				
	190	200	210	220	230
	240	250	260	270	279
m690.pep	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX				
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAA ATCCGCGCCG CCTTCAAAAT
 201 GCGGGCGCAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAATG GTGGCTTCTT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGOHNELRK IRAAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GGCGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691  97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep  VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
          |||
g691       VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
          |||

          10      20      30      40      50      60
m691.pep  IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||
g691       IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||

          70      80      90     100     110     120
m691.pep  IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||
g691       IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||

          70      80      90     100     110     120
m691.pep  IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||
g691       IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||

          130     140
m691.pep  EIQRFFHILTPQQQMWLS SCLKX
          |||
g691       EIQRFFHILTPQQQMWLS SCLKX
          |||

          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GGCGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDPQNC	DIRRLGLTQSOHNELRK				
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLNDPQNC	DIRRLGLTQGOHNELRK				
	10	20	30	40	50	60
m691.pep	IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
a691	IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
a691	IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
	70	80	90	100	110	120
m691.pep	EIQHRFFHILTPQQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQQMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

g692.seq

1	GTATCGCACA	CACGCTGTCG	CTGTTCCGAA	TCGAtacGCC	GGATTGCGC
51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	AAAATGCCGT	CTGAACACGG
101	ATGCGGTTCA	GACGGCATCA	TTTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGT	ATTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTgacGGCA	GACCAGTTGA	CATAGGCAAA
301	GCTCGGCTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTGCGCGGC
401	AGTTGTGCGG	CTTCAAGCTC	GACGATTTTG	ATGTTTTTCA	GGTTTTCCGC
451	GATGTGCGCT	TTGGATGCGG	TCAGCGGATT	GATGCCGTCT	TTGAGTTTGA
501	TCCAACCCAG	TTCGTTTCAGC	ATCACCAAGG	CGCGTCCGAA	GTTGGAcggG
551	TcgtTGGCGG	CGGATACGGT	GCTGCCGTCT	TTGACTTCTT	CCAGCGATTT
601	CAGTTTCCCC	GGATACAGTC	CCAAAGGCGC	GGTCGGCACT	TGAAGGCTT
651	CGGTGATGTC	CAGGTTGTGT	TCTTTTTTGA	AATCGTCAAG	ATAGGGTTTG
701	TGTTGGAAAG	CGTTGATGTC	CAACTCGCCC	TCCGCCAATG	CCAGATTCGG
751	GCGCACATAG	TCggTAAATT	cgaccaatTT	gacgGTGTag	cCTTTTTTCT
801	CCAGCTCGgc	tTGGATTTGT	TCTTTGACCA	TATcgccgaa	gtcgccacg
851	gTCGTGCCGA	agacgaTTTC	TTTTTTCGc	GgcCGTTAT	CGGCAGAAGG
901	GGCGGCGgca	gaggctgcGG	GCGCGCTGTC	TTTTtgaccG	ccgCAGGCTG
951	CGAGGATGAG	CGCGAGtgcg	gcggcgga	ggGTTTTGAA	GAAGGTTTTc
1001	atATTTTCTc	ctga			

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

g692.pep

1	VSHTRCRCSE	SIRRIWRNGR	EWRIKGQKCR	LNTDAVQTAS	FYTTALFGCA
51	FIPCGRVFVA	LEAFVRVGF	RVGVIGLYV	FKPLAVFVGG	FDGRFPVDIGK
101	ARLLEQGFQ	LHAAAYGVVA	VDDGKIHVGA	AARQLCGFKL	DDFDVFQVFR
151	DVGFGCGQRI	DAVFEDPTQ	FVQHHQGACE	VGRVVGGRYG	AAVFDFQRF
201	QFARIQSQR	GRHLEGFQDV	QVVFVEIVK	IGFVLEDVDV	QLALRQCQIR
251	AHIVGKFDQF	DGVAFFLQLG	LDLFFDHIAE	VAHGAEEDDF	FFRAVIGRR
301	GGRGCGRAV	FLTAAGCEDE	RECGGKGFE	EGFHIFS*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

1	GTGTTGCACA	CGCTTTGTCG	CTGTTCCGAA	TCGATACGCC	GGATTGCGCG
51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	AAAATGCCGT	CTGAACACGG
101	ATACAGTTCA	GACGGCATCA	TTTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGG	ATTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTGACGGCA	GACCAGTTGA	CATAGGCAAA
301	GCTCGGTTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTACGCGGC

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCACTT GACGGGTAG CTTTTTTTCT
801 CCAGCTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTCGCC GCGCCGTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTT TTGACCGCC CAGGCGGCGA
951 GGATGAGCGC GAGTGGCGCG GCGGAAAGG TTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

m692.pep

```

1 VLHTLCRCSE SIRRIRNRG EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF RVGVIGLVY FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVLG
151 DVRFCCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVRGYYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAV LTAAGGEDER ECGGKGFE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSES	SIRRIRNRG	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
g692	VSHTRCRCSES	SIRRIWRNG	EWRIKGQKCR	LNTDAVQTAS	FYTTALFGCA	FIPCGRVFVA
	10	20	30	40	50	60
m692.pep	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVIGLV	VFKPLAVF	VGGFDGRP	VDIGKARF	LEQGFQGLH
g692	LEAFVRVGF	ERVGVIGLV	VFKPLAVF	VGGFDGRP	VDIGKARL	LEQGFQGLH
	70	80	90	100	110	120
m692.pep	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	AATRLRGFK	LDDFVQVL	GDVRFCCG	QRIIDAVF	EFDPQFVEH
g692	VDDGKIHVGA	AAARQLCG	FKLDDFVQ	VFRDVGFG	CGQRIIDAV	FEFDPQFVQ
	130	140	150	160	170	180
m692.pep	190	200	210	220	230	240
m692.pep	VGRVVRGYYG	AAVDFDFQ	RQFQLARV	QSQRGRH	LEDFGDVQ	IVFFFEVVK
g692	VGRVVRGYYG	AAVDFDFQ	RQFQFARI	QSQRGRH	LEDFGDVQ	IVFFFEIVK
	190	200	210	220	230	240
m692.pep	250	260	270	280	290	
m692.pep	QLALSQCQIR	AYIVGKLD	QFDGVAFF	LQLGLDL	FFDHIAE	VADGRAEDD
g692	QLALRQCQIR	AHIVGKFD	QFDGVAFF	LQLGLDL	FFDHIAE	VAHGRAEDD
	250	260	270	280	290	300
m692.pep	300	310	320	330		
m692.pep	GGRSGCGGRA	VFLTAAGGE	DERECGGG	KGFEEGFH	IFSX	
g692	GGRSGCGGRA	VFLTAAGGE	DERECGGG	KGFEEGFH	IFSX	
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

a692.seq

```

1 GTGTTGCACA CGCTTGTGCG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```

```

51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGAAGACTT
651 CCGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1  VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGFV RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFGCGQRI DAVFEDPTQ FVEHHQDAGE VGRVVRGGRY AAVDFDFQRF
201 QLARVQSQR GRHLEDGFDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFFEE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

```

          10      20      30      40      50      60
m692.pep  VLHTLCRCSESIRRIIRNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFIPCGRGFVA
          |||||
a692       VLHTLCRCSESIRRIIRNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFIPCGRGFVA
          10      20      30      40      50      60

          70      80      90     100     110     120
m692.pep  LEAFVRVGFERVGVIGLGYVFKPLAVFVGFDGRFPVDIGKARFLEQGFQQLHAAAYGVVA
          |||||
a692       LEAFVRVGFERVGVIGLGYVFKPLAVFVGFDGRFPVDIGKARFLEQGFQQLHAAAYGVVA
          70      80      90     100     110     120

          130     140     150     160     170     180
m692.pep  VDDGKIHVGAATRQLRGFKLDDFVQVLDVRFVCGGQRIDAVFEDPTQFVEHHQDAGE
          |||||
a692       VDDGKIHVGAATRQLRGFKLDDFVQVFGNVRFVCGGQRIDAVFEDPTQFVEHHQDAGE
          130     140     150     160     170     180

          190     200     210     220     230     240
m692.pep  VGRVVRGGRYGAADFDFQRFQLARVQSQRGRHLEDGFDVQIVFFFEVVKIGFVLEDVDV
          |||||
a692       VGRVVRGGRYGAADFDFQRFQLARVQSQRGRHLEDGFDVQIVFFFEVVKIGFVLEDVDV
          190     200     210     220     230     240

          250     260     270     280     290     300
m692.pep  QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDFFRRAVVG
          |||||
a692       QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDFFRRAVVG
          250     260     270     280     290     300

          310     320     330
m692.pep  RSGCGGRAIFLTAAGGEDERECEGGGKGFEFGFHIFSX
          |||||
a692       RSGCGGRAIFLTAAGGEDERECEGGGKGFEFGFHIFSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

g694.seq

```
1 TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51 AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GcaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGACTGTT CGGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTTCG ATAGCAGATG TCTTCCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCCCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCCGCGCGT TCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CCAGTGTGCG GCCCGCGGCG ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 CGGCACATAA ACCGGCGCGC CGAATTCCTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTC CGTTCATAAG TTTTGCATTG CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

g694.pep (partial)

```
1 SAFVLPHKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPPFAHG
51 FMPPSAYGCG YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHOR ASRIKYPETA
251 LRRFLLHRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQV HDEFVVDDEV
301 AHINRRAEFF QSTFDNTDCP IHTGAEEAARI GKDDGFSVHK FCIPCSGDIH
351 VFLXLCDGR YCQAPPTPHR RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

m694.seq

```
1 TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51 GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTGCTCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAATCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCAGC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

m694.pep

```
1 LVASASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFA LAAQLFGODE
51 HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
```

```

151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVUN DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

m694.pep      10      20      30      40      50
LVSASGTRQKCR LKPVTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694          10      20      30      40
SAFVLPKHPMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR

m694.pep      60      70      80      90     100     110
TLAFAYGFVPPSAYGCGYFPHQHFGGRGRACRYADVFVALKPCALQVACIIHHIRIDSARC
g694          50      60      70      80      90     100
APPFAGHGFMPPSAYGCGYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVVHHIRIDSARC

m694.pep     120     130     140     150     160     170
RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694         110     120     130     140     150     160
RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV

m694.pep     180     190     200     210     220     230
FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
g694         170     180     190     200     210     220
FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAACKLPKRAFDLGVPLMPDHDDFT

m694.pep     240     250     260     270     280     290
VLGIQSGDFLMHFRHQASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694         230     240     250     260     270     280
VLGIQSGDFLMHFRHQASRIKYPETALRRFLHLRLRYAVCRINQCRARRHFRQVFDKHR

m694.pep     300     310     320     330     340     350
TFFTQVVHDEFVUNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694         290     300     310     320     330     340
AFFAQVVHDEFVVDDEFVAHINRRAELFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI

m694.pep     360     370     380
SFSDGINIFLLGFYGGRCCTPTPPTPHRRRX
g694         350     360     370
PCSDGIHVFLXXLCDGRYCAQPTPHRRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

a694.seq

```

1  TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTC
51  GACGCGATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTGG GCAGGACGAA
151 CACAAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCGTCCG TTACGCGGAC TTTGTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATACAGATGT CGCACTGTTT TGCCAACCTT TGACGGCGG TTTGCCGGTT
451 GGTCTGCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG

```

```
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGTTGTGTC ACACGAAT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGCGCGGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCTC
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

a694.pep

```
1 LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51 HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRIADI FLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLYAVCRIN QCRARRHFRO VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCGG AGGGCAGCCG AACCAGAAATG
301 CGGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 CCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAAATA
451 CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCNSQRF QSKPAERYAD
51  CPHPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVPEGSRTM
101 TPQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCGG CAGGCAGCCA AACCAGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CTTGTTGAAA GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHRRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
g695	10	20	30	40	50	60
	LPQTRPARRHRRQYFVERKGDARSGFXCAAQCONSQRQFQSKPAERYADCPHHPARRRR					
m695.pep	70	80	90	100	110	120
	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	70	80	90	100	110	120
	FDPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTMPTQENASDGIPYPVPTLQDR					
m695.pep	130	140	150	160	170	180
	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDRLKLEHYLNTTEGGSASA					
g695	130	140	150	160	170	180
	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDRLKLEHYLNTTEGGSASA					
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAASLLKGADGGDGGGSAQRSMYLLQLSRARMGNCS					
g695	190	200	210	220	230	240
	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSAQRSMYLLQLSRARMGNCS					
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
m695.pep	AVRKRX					
g695	AVRKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

```
a695.seq
1  TTGCCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAATATTT
51  TGTTGAACGG AAGGGTGATG CGCGAAGCGG CTTCGGATGC GCCGCCCAGC
101  GTCGGCATCC TCAAAGATTT TAATCAAAAC CTGCCGAACG ATACGCCGAT
151  TGTCCCATC ACCCTGCCCG TCGCGACGG TTGACCTG CTTCTGAAAA
201  AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251  CCGCCTGTTT TCCCTGTT TCCCGCAATA TTCAGGATAT GCGGCTCGAA
301  CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTTCACAC
351  TCTGCAAGAC CGTTTGGATT ATCTGGAAGG CACACTCGTC CGCTGTCTGA
401  ACGAAGTGGA AACCTTAAAC GGCAAGTCA AAGCACTGGA GCATGCGAAA
451  ACACACCCTT CCAGCAGGGC ATACGTCCAA AAACCTGACG ACCGCAAGTT
501  GAAAGAGCAT TACCTCAATA CCGAAGGCGG CAGCGCATCC GCACATACCG
551  TCGAAACCGC ACAAACCTC TACAATCAGG CACTCAAACA CTATAAAAGC
601  GGCAGGTTTT CTGCCCTGTC CTCCTGTTG AAAGGCGCGG ACGGAGGCGA
651  CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701  CGCGTATGGG CAACTGCGAA TCCGTATCG AAATCGGAGG GCGTTACGCC
751  AACCGTTTCA AAGACAGCCC AACCGCGCCT GAAGCCATGT TCAAAATCGG
801  CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAGG GCGACTTGCC
851  GCAGCCTGAT ACAGACCTAT CCCGCGAGCC CGGCGGCAAA ACGCGCCGCC
901  GCAGCCGTGC GCAAACGATA G
```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

```
a695.pep
1  LPQACPARRH HCHRQYFVER KGDARSGFRC AAORRHQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSAACSSPV SRNIQDMRLE
101  PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151  THPSSRAYVQ KLDDRKLKEH YLNTTEGGSAS AHTVETAQNL YNQALKHYKS
201  GRFSAAASLL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251  NRFKDSPTAP EAMFKIGECQ YRLQKDIAR ATWRSLIQTY PGSPAAKRAA
301  AAVRKX*
```

Computer analysis of this amino acid sequence gave the following results:

m695/a695 88.3% identity in 308 aa overlap

BNSDOCID: <WO 8957280A2 | >

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAA GCGCAGACTC GGCGGCAGAA
251 GCCGCACTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

a696.pep

```

1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFNL
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

m696/a696 100.0% identity in 120 aa overlap

```

m696.pep      10      20      30      40      50      60
               LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGF
a696           LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGF
               10      20      30      40      50      60

m696.pep      70      80      90      100     110     120
               ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFNL
a696           ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFNL
               70      80      90      100     110     120

m696.pep      X
a696           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

g700.seq

```

1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTTCG
151 CGCGTGGAGG ATTTGGGTTT CCGGTTGGGC GATATGGCGT TGACGGTTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCAGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTAATGACCG AGGCTTACCG
651 GCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGCGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC GGATGCGGCG
751 GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTCCGGGC GGTTTGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCCG TTTCTGATGG TGGTGTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

g700.pep

```

1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLPW RIGGKKGVS
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSM DFTLPVIQAG GLEVPVAVS FGVVNVIAAP FLMVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

```

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51 ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCGGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCT
151 CGCGTGGAGG ATTTGGGTTT CCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATTCGGC AAACGTATGC GCGATATTG GATGCCGCT GAAAGCGCGG
401 GCATGTATTG TCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
501 GTTGTGGTTC TGGTTTATGC TTTCATCTCT TTCGGGCGGG CTGCTGTTTG
551 CCGCATCGAC AGACGGTGTG TCGTGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTCATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTCC AGATGCGGCG
751 GTGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
801 GGGTGCGGGC GGTGTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTC TCCTTTGGGT
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

```

1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLF PWRIKKGKGV
101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMP ESAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL VNRGIRLSV WFMSSLSGG LLFAASTDGV SWTKGLAMAS
201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSM DFTLPVIQAG GLEVPVAVS FGVVNVIAAP FLMVVFSA
301 *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLF PWRIKKGKGVSVGVSGSVGQLGCVLLGFAFG					
g700	DMALTVLWLFVCTVGANLLALAVLGKLS PWRIKKGKGVSVGVSGSVRQLGCVLLGFSVG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFMSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300

m700.pep	X
g700	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1   ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTATC  CGTGTGCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCT
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATCCCGTGG CCGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGTGTGT  CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAA
451 AGCAGCGGCG TATCGTTGCG GCAGTTTTG GTCAACCGCA GGGGTATTCG
501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GTTATCCCT  CTCGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGA CGATTGGCA  CGAGAGCTGT
701 TCGCGCTGGC ATTATTCCG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGGTG  GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTTC
801 GGGTGCGGGC GGCTTGAAG  CCGTACCGGT AGCGGTGAGC TTCGCGGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTTTT CGCTTTGGGC
901 TGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1   MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLF PWRIKKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQL
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYLSLGL VMTEAYGAVW GSIALLNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *
  
```


m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLRVEDLGSRLD					
	10	20	30	40	50	60

	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120

	130	140	150	160	170	180
m700.pep	KLMRDIWMPSEAGMYCLMLLVFLIGVQLKSSGVSIRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSEAGMYCLMLLVXIGVQLKSSGVSIRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

	190	200	210	220	230	240
m700.pep	LLFAASTD	GVSWTKGL	AMASGFGW	YSLSGLM	TEAYGAV	WGSIMLLN
	:	:	:	:	:	:
a700	LLFAASAD	GVSWVKGL	AMASGFGW	YSLSGLM	TEAYGAV	WGSIALLN
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPD	AAVGVGG	ATSMDFTL	LPVIQGA	GGLVVPV	AVSFGVVV
	:	:	:	:	:	:
a700	LLMKRFPD	AAVGVGG	ATSMDFTL	PVIRGAG	GGLVVPV	AVSFGVVV
	250	260	270	280	290	300

m700.pep	X
a700	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACCG CTTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAAACCTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCACTC TTTCGCCGGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCCA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCTGTC GCGGACACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VWVAPNSFAG
51  FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GGTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACCG CTTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC SGTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHV	AGIPTAS	MAQSTP	PSSPTMA	KTCLDTS	PEAGLM
	:	:	:	:	:	:
g701	MSWHIFQV	AGIPTAS	MAQSTP	PSSPTMA	KTCLET	SPEAGLM

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```

          10      20      30      40      50      60
          70      80      90     100     110     120
m701.pep  MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g701      IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISLTLSC
          70      80      90     100     110     120

          129
m701.pep  SGTRLLSAX
          :|||||
g701      GGTRLLSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```

a701.seq
  1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
 51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101  CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151  TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201  CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251  TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301  TGTGCGGTCT GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351  GTTGTCGGGC AGCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```

a701.pep
  1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
 51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101  CAVGKASLNN RATSSLTLSG SGTRLLSA*

```

m701/a701 92.2% identity in 128 aa overlap

```

          10      20      30      40      50      60
m701.pep  MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSSISQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a701      MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSSISQT
          10      20      30      40      50      60

          70      80      90     100     110     120
m701.pep  MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a701      MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSC
          70      80      90     100     110     120

          129
m701.pep  SGTRLLSAX
          ||||||
a701      SGTRLLSAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```

g702.seq
  1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
 51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCTGTGA
101  AATCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151  TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201  TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251  TTTGAGGGT GGGGATGCCG CTTTCGACAA GGGCGCGGGA CAAATCGACG
301  GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAATG CGCCGGCGGT
351  CAGGATTTTC cggggggtca gttga

```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

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```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVPPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCCAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP					
	:					
g702	MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCKPGLMAKTAPASSTALSCSGLVTVPPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSM AVLKSSIAITGTTAPAVKIS					
	:					
g702	MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAITGTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVLRVEWGILLRWDRXL					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCCAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
|||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m702.pep  TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
|||||
a702      TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
              70      80      90      100     110     120

              130     140
m702.pep  RGVSLDISVLRVEWGILLRWDR LX
|||||
a702      RGVSLDISVLRVEWGILLRWDR LX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTGc gctGTTgggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVND SREV
251 KVPSFDEMKG QIAGNLQAE R IDRVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVA AAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVA AAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLD RSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTTVVAQEVKRLKLD RSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILT DKEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILT DKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTGCGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCCTCCTT CAAAACCGTT TGGCAGGCGG TAAATATATGG
351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CCGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAEI IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVVKVPSFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
a703	VYYVNSREVVKVPSFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251 TGGAAACCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAATCAGG
451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCGC TGCCGACCTA CCTTTACGGC
601 GCGGACATCG AACCCGATTT CTGCAAAATC CTCCATTGGG GCGGCTTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
701 CGTGCGCGCA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

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801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCG ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGGCG
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCGGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCTCG CCCAAACACG CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCGG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GGCAGAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAAA CAGAAGGCGG
1851 GCGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGCGGCT GCGGAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CAATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGACGGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAATGCCG TCCGAACAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```
a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLGSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLE QQLLRDGI V RIDLNYSTHR CRVWDDGKI RLS DILLKIR
151 QIGYTAAPYD AQKIEANQK ERQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFYCAVPF YQGAIRD LKN RRVGMDPTIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTOETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAELAEQYAS SFIFGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLG YVQPIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*
```

m704/a704 99.8% identity in 823 aa overlap

```
105 20 30 40 50 60
m704.pep MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
|||||
a704 MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
10 20 30 40 50 60

70 80 90 100 110 120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLEQQQLLRDGI
|||||
a704 ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLEQQQLLRDGI
```

1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA				
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN				
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMYFESIAMLLFFLLGGRFMEHIARRKAGD					
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV					
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRITGGGTRLSHIVRLLDRLAQAQKPR					
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAELEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSLATPTAL					
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLAQTTDII FDKTGTLTQGKPAVRRISLLRGTDFAFVLA					
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR					
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYLSQSGFQAVFYLTDPKDSAAEAVRQLAGKNLTLHIL					
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAEARALGVAHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD					
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHII RQNLWAGAYNIIAVPLA					
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSSLAVLGNALRLHKGKMQSEKMPSEQX					
	790	800	810	820		

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

BNSDOCID: <WO 9957280A2 | >

```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100     110     120
m705.pep  ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180
g705      ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230     239
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGGC GATTATGCCC GCCGGCGGCA TCGTGCAGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
651 TTGTAAAGTG CTGTCCTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLQV IVFYGLPSVG
101 IYIDFIPAAI IGFSNLVNGAY ASETIRAAIL SVKPGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFRDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep  10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||
m705      10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||

a705.pep  70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||
m705      70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||

a705.pep  130     140     150     160     170     180
ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||
m705      130     140     150     160     170     180
ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||

a705.pep  190     200     210     220     230     239
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
|||||
m705      190     200     210     220     230
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
|||||

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```
1 ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAatgaCCGT CTTCGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cggtgGAacg taTGctcggg acggtcacg
251 ggctgGGCGC GGGTTTGGgc gTTTATGGC TGAACCAGCA TTAttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCCGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCCG
501 CGCCAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAAGC TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```
1 MNSSQRKRLS GRWLNSYERY RHRLIHAVR LGGTVLFATA LARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```
1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGATAG GGATACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCCGCAAAA ACGGCTACGT CCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAAGC CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```
1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
```

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRWLDAHE ROHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

m706.pep	10	20	30	40	50	60
	MNTSQNRNLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQKRRLSGRWLSYERYRHRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
m706.pep	70	80	90	100	110	120
	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTSALAGWAA					
g706	LGMLQFQGAIYSNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTSALAGWAA					
	70	80	90	100	110	120
m706.pep	130	140	150	160	170	180
	VGKNGYVPMLAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
m706.pep	190	200	210	220	230	240
	FMLADNLADCSKMAIEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	FMLADNLADCSKMAIEISNGRRMTRERLEQNMVKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
m706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLOSPKLNSEIRLLDRHFTLLQTDLOQTVALING					
g706	SMMEAMQHAHRKIVNTTELLLTAAKLOSPKLNSEIRLLDRHFTLLQTDLOQTAALING					
	250	260	270	280	290	300
m706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRWLDAHE					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRWLDAHE					
	310	320	330	340	350	360
m706.pep	370					
	ROHLRQSLLETREHGX					
g706	ROHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCC GGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTTATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCCG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGTTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAAGC	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCAC
751	CGTAAATTTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

901 AGACACGCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
 1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

a706.pep
 1 MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
 151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLDC SKMIAEISNG
 201 RRMTRERLEE NMAKMRQINA RMVKSRS LA ATSGESRISP AMMEAMQHAH
 251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
 301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHS*

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
m706	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
a706.pep	70	80	90	100	110	120
	LGMLQFOGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG					
m706	LGMLQFOGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG					
a706.pep	130	140	150	160	170	180
	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAL LPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAL LPLKSTLMWR					
a706.pep	190	200	210	220	230	240
	FMLADNLDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS LA ATSGESRISP					
m706	FMLADNLDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS LA ATSGESRISP					
a706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
a706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTRRKWLDAHE					
a706.pep	370					
	RQHLRQSLLETREHSX					
m706	RQHLRQSLLETREHGX					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```
1 ATGGAAATTA TTAACGATGC AGAAGTTATC CGTTCCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTTGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAA CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGCG AGCAGAATAA ACCCATACGG TCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTT ATATGGACGC
751 GGTTTGCGCG ACAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCTAT TCGGTGCCG GTAAAAAAT
851 GGCTGTTTTC TTTAATCAC AATGGACAT GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCGGAG CGCATGCTTT GGCCTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGC CATGCCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCGGCC CCATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCGGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGGCG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAAGAGG GGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGCAAGGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```
1 MEIINDAELI RSMQROQHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQL
101 IVRGYLTSQA IIQPNMDSG ILKLRVSAGE IGDRIYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEGKSDLQ
201 IKWQONKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRA Y LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAEA PFILGKQOFF YATAIQAWN KTPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQWNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```
1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAAATCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAAACC TGCGTCGTTT GCCGAGTGT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTCAAG ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG
```

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPONMDSGIL
51  KLRVSAGEIG DIRYEKRDY KSAEGSISAF NNXPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYGKQ YQSSLAERM
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHRAYLX
301 RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPXXSRMKII TAGLDAAAPX
351 MLGKQOFFYA TAIQAOWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGRFGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep
10 20 30
XKETAFKTMCLGSNNLSRLQKAAQQILIV
|||||
m707
50 60 70 80 90 100
EDETPTCRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIV

a707.pep
40 50 60 70 80 90
GYLTSQAIQPONMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNXPLYRNKI
|||||
m707
110 120 130 140 150 160
GYLTSQAIQPONMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKFPYRNKI

a707.pep
100 110 120 130 140 150
LNLRDVEQGLNLRRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||||
m707
170 180 190 200 210 220
LNLRDVEQGLNLRRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT

a707.pep
160 170 180 190 200 210
GKYQGNVALSXDNPLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||||
m707
230 240 250 260 270 280
GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK

a707.pep
220 230 240 250 260 270
WLFSEFNHNGHRYHEATEGYSVNYDYGKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
|||||
m707
290 300 310 320 330 340
WLFSEFNHNGHRYHEATEGYSVNYDYGKQYQSSLAERMLWRNRLHKT SVGMKLWTRQTY

a707.pep
280 290 300 310 320 330
KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTGMRQSM PAPEENGSGTI
|||||
m707
350 360 370 380 390 400
KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTGMRQSM PAPEENGSDIL

```

```

340      350      360      370      380      390
a707.pep PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
| : |||||: ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m707      PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m707      EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA  AGCCATCCAA  ACGAATCTCT  TTATTACTTG  TTCTTGCCCT
51  GGGCGGTGCG  AGCATCTCTT  ACCGCCCTCC  GCGGGCAGAA  AAAGCCCAATC
101 AGGTTTCCAA  TATCAAAACC  CAGTTGGCGA  TGGAAATATAT  GCGCGGTGAG
151 GACTACCGTG  AGGCAACGCG  AAGTATTGAA  GATGCCTTGA  AATCGAAACC
201 TAAAAACGAA  CTTGCTTGGC  TGGTCCGCTG  CGAAATCTAT  CAATACCTGA
251 AAGTTAACGA  CAAGGCGCAG  GAAAGTTTCC  GGAAGCCCT  CTCCATCAAA
301 CCCGACAGTG  CCGAAATCAA  CAACAACCTAC  GGCTGGTTCC  GTGCGGCGAG
351 GCTCAACCGC  CCTGCCGAAT  CTATGGCATA  TTTTCGACAAA  GCCTGTGCGG
401 ACCCCACCTA  CCGGACCCCT  TATATTGCCA  ACCTGAATAA  AGGTATATGC
451 AGCGCAAAAC  AGGGGCAATT  CGGATTGGCG  GAAGCTTATT  TGAACGCTG
501 CCTCGCGCGC  CAGCGCGAGT  TCCCAACCGC  ATTAAAGAA  CTGGCGCGCA
551 CCAAAATGCT  GGCCGGGCG  TTGGGCGGAT  CCGATTACTA  TCTTAAAAAA
601 TACCAAGACA  GGGTAGAAGT  CCTCAGGCC  GATGATTTGC  TGCTAGGCTG
651 GAAATTGGC  AAAGCCCTCG  GCAACGTGCA  GCGGCATAC  GAATATGAAG
701 CACAATTGCA  GGCAAAATTC  CCTACTCGG  AAGAATTGCA  AACCCTCCTC
751 ACCGTCAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MPFKPSPKRIS  LLLVLALGAC  STSYRPSRAE  KANQVSNIKT  QLAMEYMRGQ
51  DYRQATASIE  DALKSNPKNE  LAWLVRAEIY  QYLKVNDKQA  ESFRQALSIK
101  PSDAETNNNY  GWFLLCGRLLR  PAESMYFDK  ALADPTTPTP  YIANLKGKIC
151  SAKQGQFGLA  EAYLKRSLAA  QPQFPFAFKE  LARTKMLAGQ  LGDADYFFKK
201  YQSRVEVLQA  DDLLLGWKIA  KALGNVQAAY  EYEAQLQANF  PYSEELQTVL
251  TQO*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```
m708.seq
1  ATGCCTTTTA  AGCCATCCAA  ACGAATCTCT  TTATTACTCG  TTCTTGCCTT
51  GGGCGCGTGC  AGCACTTCCT  ACCGCCCTC  CGCGGCAGAA  AAAGCCCAATC
101 AGGTTTCCAA  TATCTAAACC  CAGTTGGCAA  TGGAAATAT  CGCGGTCAGC
151 GACTACCGTC  AGGCACGGC  AAGTATTGAA  GACGCCCTGA  AATCGGACCC
201 TAAAAACGAG  CTTGCTTGGC  TGGTCCGCTG  CGAAATCTAT  CAATACCTGA
251 AAGTTAAACG  CAAGCGCGAC  GAAAGTTTCC  GCGAAGCCCT  CTCCATCAAA
301 CCCGACAGTG  CCGAAATCAA  CAACAAC TAC  GGTTCGGTCC  TATCGCGCAG
351 GCTCAACCGC  CCTGCCGAAT  CTATGGCATA  TTTGACAA  GCTCTGGCCG
401 ACCCCACCTA  CCGGACCCCT  TATATTGCCA  ACCTGAATA  AGGCATATGC
451 AGCGCAAAC  AGGGGCAATT  CGATTGGCG  GAAGCTATT  TGAACGCTG
501 CCTCGCCGCG  CAGCCGCGAG  TCCCAACCGC  ATTTAAAGAA  CTGGCGCGCA
551 CCAAAATGCT  GGCCGGGCG  TTGGCGGATG  CCGATTACTA  CTTTAAAAAA
601 TACCAAAGCA  GGGTAGAAGT  CTTGACGCC  GCGATTTCG  TGCTAGGCTG
651 GAAATATTGC  AAAGCCCTCG  GCAACGCACA  GGCGGCATAC  GAAATATGAAG
701 CACAATTGCA  GGCGAATTT  CCTACTCGG  AAGAATTGCA  AACCGTCTC
751 ACCGGTCAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pgp

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||||
g708           MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRLNR
              |||||
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRLNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE
              |||||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
              |||||
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51 GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGCGAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTGCGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCGAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIIYQYLKVNDKAQESFRQXLSIKPDSAEINNXYXWFLCGRNLNR					
m708	DALKSDPKNELAWLVRAEIIYQYLKVNDKAQESFRQALS IKPDSAEINNXYGWFLCGRNLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFAFKE					
m708	PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLL GWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLL GWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

1	ATGTTTGCTT	TCAAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCACTTGC
51	CGTCGTCGTC	GCTCTGATTG	CCGCAATGGG	CTATACCATC	ATTTCATTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTCGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAAATACAAC	GATATGCAGG	CAGGGATGAT
201	AGGCGCGTTG	AATCAGGGA	TGGGCGCGGT	TTACCTGTTT	TTCTTCATCG
251	GGCTGATGGT	CAGCGCGCTG	ATGATGAGCG	CGCGGATTCC	GACGCTGATG
301	TATTACGGTT	TCGGGCTGAT	TTCCCGGACT	TATTTTATT	TTTCCGCCTT
351	CGCGCTGTGT	TCCGTATCG	GCGTGTCCAT	CGGCAGCAGC	CTGACCGCCT
401	GCGCCACTGT	CGGCGTTGCC	TTTATGGGGA	TGGCGGCGGC	GTTTCAGGCC
451	GATATGGCGA	TGACGgcggg	cgcgattgTT	tccggTGTGT	TTTTCGGCCA
501	TAAAATGTCC	CGGCTTTCCG	ACACCACGGG	CATTTCGCG	TCCATCGTCG
551	GTATCGACCT	GTTTGAACAC	ATCAAAAACA	TGATGTACAC	CACCATCCCT
601	GCGTGCGTTA	TCAGCGCGGC	ACTGATGCTT	TGGCTTCTTC	CCAGCGTCGC
651	CGCGCAGGAT	TTGAACAGCG	TCGAATCCTT	CCGCAGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GACGCGCTAT	TCGCTGATTG	CGTTTGCACT	GTTGGTCTGT
751	TTGGCATTGA	TGCGCGTCAA	TGCCGTGGTC	GCCATGCTCT	TTACCGTCAT
801	TGCCGCCGTT	GCGGTAACGT	ATCTGCACAG	CACGCCCGAT	CTGCGTCAGC
851	TCGGCGCGTG	GTTTATGGC	GGCTACAAAC	TCGAAGGCGA	AGCGTTTAAA
901	GACATTGCCA	AACTGATTTC	GCGCGGCGGC	TTGGAGAGTA	TGTTCTTTAC
951	GCAGACCATC	GTTATCCTCG	GTATGAGTTT	GGGCGGGCTG	CTGTTTGCGC
1001	TCGGTGTGAT	TCCTTCCTTG	CTGGAGGCGG	TCCGTACCTT	CTTGACGAAT
1051	GCCGGACGCG	CGACGTTTCA	CGTTGCCATG	ACTTCGGTCG	GGGTCAATTT
1101	CCTGATTGGA	GAGCAATATT	TGAGCATCCT	GCTTTCGGGA	GAAACGTTCA
1151	AACCCGTTTA	CGACAACTC	GGCCTGCATT	CGTGCAACCT	GTCGCGGACT
1201	CTGGAAGATG	CGGGGACGGT	GATTAACCCG	CTCGTGCCGT	GGAGCGTGTG
1251	CGGCGTATTT	ATCAGCCACG	CCCTTGGCGT	ACCCGTTTGG	GAATATCTGC
1301	CTTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTAACCTT	GTTATTCGGC
1351	TGGACGGGGC	TGACTTTGAG	CAAAAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

1	MFAFKSLDDM	PRGEALAVVV	ALIAAMGYTI	ISLEWLPHMS	IIAAIVVLIL
51	YGLARGLKYN	DMQAGMIGAL	NOGMGAVYLE	FFIGLMVSAL	MMSGAIPTLM
101	YYFGFLISPT	YFYFSAFALC	SVIGVSISS	LTACATVGVA	FMGMAAFOA
151	DMAMTAGAIV	SGVFFGDKMS	PLSDTTGISA	SIVGIDLFEL	IKNMMYTTIP
201	AWLISAALML	WLLPSVAAQD	LNSVESFRSQ	LEATGLVHGY	SLIPFALLVV
251	LALMRVNAV	AMLFVTIAAV	AVTYLHSTPD	LRQLGAWFYG	GKLEGEAFK
301	DIAKLISRG	LESMTFTQTI	VILGMSLGL	LFALGVIPSL	LEAVRTFTLN

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
451 WTGLTSLSK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
1 ATGTTTCGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTCTCTCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTCCGCGT TCCATCGTCG
551 GCATCGACTT GTTGTAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTTCG
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTGCGCT GTTGCTCATT
751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCCCCAT CTGCGTCAGC
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTGCGC
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA
1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTCCGGGACG
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCTT TTTCTGCTAT TTGAGTTTGG CTTGACCCTT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
1 MFAFKSLLDL PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQQGMIGAL NOGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGGLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFHE IKNMYYTTIP
201 ARLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DVVKLISRGG LESMFTQTI VILGMSLGL LFALGVIPSL LEAIRTFLT
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
451 WTGLTSLSK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLLDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLLDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNOGMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSSFALC					
g709	DMQAGMIGALNOGMGAVYLF FFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSAFALC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVA FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVA FMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m709.pep	SIVGIDLFHEIKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMYYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFVMAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVAMLFVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
g709	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTLTEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSCNLSRTLTEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX					
g709	ISHALGVVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1   ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCGTCATCG GCGTGTCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TNTTNGGCGN
501 CAAAATGTCN CCGCTTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCTG
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCCTT GTTGCTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTNGG GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCANCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1   MFAFXSLDM PRGEALAVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMOQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGGISPT YFYFSAFALC SVIGVSIGSS LTTTCATVGA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXA SIVGIDLFEH IKNMYYTTP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLV
251 LALMRVNAV AMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQTI VILGMSLGG LFFALGAIPL LDAVRSFLT
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

a709.pep	MFAFXSL	DMPRGEALAVV	VVALIAAMGYTII	XLEWLP	HMSIIAAIV	VLILYGLARGLKYN
m709	MFAFKSL	DMPRGEALAVV	VVALIAAMGYTII	SLEWLP	HMSIIAAIV	VLILYGLARGLKYN
a709.pep	DMQQGMIGALN	QGMGAIY	FFFFIGLMVS	ALMMSGAI	PTLMYYG	FGLISPTYFYFS
m709	DMQQGMIGALN	QGMGAIY	FFFFIGLMVS	ALMMSGAI	PTLMYYG	FGLISPTYFYFS
a709.pep	SVIGV	SIGSSLTTCAT	VGVA	MGXXXAF	XAMXXXXX	IVXXAXGXKMSPLSDTXG
m709	SVIGV	SIGSSLTTCAT	VGVA	FMGMAAFQ	ADMAMTAGAIV	SGAFFGDKMSPLSDTTGISA
a709.pep	SIVGID	LFEHIKNM	MYTTIPAW	LISXXLM	LXLLPSVAAQ	DLNSVESFRSQLEATGLVHCY
m709	SIVGID	LFEHIKNM	MYTTIPAW	LISAALML	WLLPNVAAQ	DLNSVESFRSQLEATGLVHG
a709.pep	SLIPF	ALLVVLAL	MRVNAV	VAMLF	TVIAAV	AVTYLHSTPDLRQLGAWFYGGYKLEGEAXX
m709	SLIPF	ALLVILAL	MRINAV	VAMLF	TVMVAV	AVTYLHSTPDLRQLGAWFYGGYKLEGEAFK
a709.pep	DIAKL	ISRGGLESM	FFTQTIV	ILGMSL	GGLLFAL	GAIPSLDAVRSFLT
m709	DVVKL	ISRGGLESM	FFTQTIV	ILGMSL	GGLLFAL	GVIPSLLEAIRFTLT
a709.pep	TSVGVN	FLIGEQYLS	ILLSGET	FKPVYDK	LGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF
m709	TSVGVN	FLIGEQYLS	ILLSGET	FKPVYDK	LGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF
a709.pep	IXHAL	GVPVWEY	LPYAFFCY	LSLALT	LLFGWT	GTLTSLSKKX
m709	ISHAL	GVPVWEY	LPYAFFCY	LSLALT	LLFGWT	GTLTSLSKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGA	AACCC	ACGAAAA	AAT	CCGCCT	GATG	CGCGA	ATTGA	ATAA	TGGTC
51	CCAGG	AAGAT	ATGGC	GGA	AGCTG	GCGAT	GTCGC	CAGGC	GGGT	ATGCCA
101	AAATC	GAACG	GGGCG	AAACG	CAGTT	AATA	TCCCG	CGTTT	GGAG	CAGTTG
151	GCTCA	GATTT	TCAAA	ATCGA	TATGT	GGGAC	TTGCT	CAAAT	CGGG	CGGTGG
201	TGGGA	TGGTG	TTTCA	GATTA	ATGA	AGGTGA	TAGTG	GTGGC	GATAT	TGCGT
251	TGTAT	GCGTC	GGGTG	ATGTT	TCGAT	GAAAA	TAGA	ATTTT	AAAA	TGGAG

301 TTGAAACACT GCAAAGAAAT GTTGAACAA AAAGACAAAG AAATCGAGCT
351 GCTCCGCAAG CTGACCGAAA CCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 2386; ORF 710>:

```
m710.pep
      1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
     51  AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
    101  LKHCKEMLEQ KDKEIELLRK LTETV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2387>:

```

a710.seq
1  ATGGAACCC  ACGAAAAAT  CCGCCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGGCAGGC  GGGTATGCCA
101 AAATCGAACG  AGGCGAAACG  CAGTTGAATA  TCCCGCGTTT  GGAGCAGTTG
151 GCGCAGATTT  TCAAATTGA  TATGTGGGAC  TTGCTCAAAT  CGGCGCGCGG
201 CGGGATGGTG  TTGCAGATT  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATG
301 GAATTA AAC  ACTGTAAAGA  ATGTTGGAA  CACAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A

```

This corresponds to the amino acid sequence <SEQ ID 2388; ORF 710.a>:

```

.a710.pep
      1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
     51  AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
    101  ELKHCKEMLE HKDKIEILLR KLTETV*

```

a710/m710 85.7% identity in 126 aa overlap

```

      10          20          30          40          50          60
a710.pep    METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD
             |||||
m710        METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD
             10         20         30         40         50         60


      70          80          90         100         110         120
a710.pep    LLKSGGGGMVLQINDVDTSNGEFAYTAQDASGKAGFVKMLKHCKEMLEHKDKIEILLR
             :||::: |:| :::: |::: ||::::|:::|:|||||
m710        LLKSGGGGMVFQINEGDVG-DIALYASGDVSMKIEFLKMELKHCKEMLEOKDKIEILLR
             70         80         90         100         110
```

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTGGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTREPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDTYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRDLIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```
1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTDD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

a711/m711 99.8% identity in 431 aa overlap

	10	20	30	40	50	60
a711.pep	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
m711	70	80	90	100	110	120
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
m711	130	140	150	160	170	180
a711.pep	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
m711	190	200	210	220	230	240
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTDD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTDD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
m711	250	260	270	280	290	300
a711.pep	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKQRLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
m711	310	320	330	340	350	360
a711.pep	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
m711	370	380	390	400	410	420
a711.pep	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

430

1149

a711.pep

AKFMAKKKVLKX

m711

|||||||
AKFMAKKKVLKX

430

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
  1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
  51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTGTGCCGC
 101  AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
 151  CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
 201  TTTGTTCCGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
 251  CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
 301  GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
 351  GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
 401  TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
 451  ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
 501  TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
 551  CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
 601  GCGCGTGCCA AAAATGCCGA CATTGCCACG GCCTTGTCCA AAGTGGCGGG
 651  CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
 701  AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
 751  GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
 801  CGTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
 851  GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGTGTTG
 901  GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
 951  GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001  ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051  CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101  CGACCCGGCA CTAATCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151  GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201  AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGCTGAT
1251  TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301  AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351  ATCCCGGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401  TTTGATTTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
  1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
  51  QPALEPVQLF SDAEADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
 101  AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
 151  ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
 201  GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
 251  GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
 301  AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
 351  QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
 401  SDRLLPKVKS EILDVLIKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
 451  IPADVINGLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAACAA CCCCCTTTG GGCAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGCGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSESCSE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKWVYK PTMTLHRPKT
251 VVVSADADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGVWLQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGCGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDV VIGRLGPEAA
51 IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMIDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLDKVVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGKR KGVSHKGKKG GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
m713	10	20	30	40	50	60
a713.pep	70	80	90	100	110	120
m713	70	80	90	100	110	120
a713.pep	130	140	150	160	170	180
m713	130	140	150	160	170	180
a713.pep	190	200	210	220	230	240
m713	190	200	210	220	230	240
a713.pep	250	260	270	280	290	300
m713	250	260	270	280	290	300
a713.pep	310	320	330	340	350	360
m713	310	320	330	340	350	360
a713.pep	370	380				
m713	370	380				

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
  51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
 101  TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
 151  CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
 201  CCGTACGGGC AAAAACCGCC AGCACCGTGT GTTGGCCGTC ATGGCCAAGC
 251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
 301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
 351  TGTAACCGC GCGGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
 401  GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
 451  GGTATCTCGG CCGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
 501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
 551  CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
  51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
 101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
 151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
  51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
 101  TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
 151  AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
 201  CCGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGGCCGTC ATGGCCAAGC
 251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
 301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
 351  TGTAACCGC GCGGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
 401  GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
 451  GGTATCTCGG CCGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
 501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
 551  CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
  51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
 101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
 151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPRSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	:					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEIIMVWHVNVVRGGNNRITRFRAAGDRLTDYSDAVIESLFNRLKPAHTA					

1154

m714 AGDRLAPQEIIMVWVHVNRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq

```

1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep

```

1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*

```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
	: : : : :					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGASKSAEGSCGASKSAEG					
	10	20	30	40	50	60
	60	70	80	90	100	
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	: : : : : :					
g716	SCGAAASKAGEGKCGEGKCGATVKKAKHHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq

```

1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep

```

1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*

```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	: : : : :					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	: : : : :					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq

```

1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAC  CCTGTTCCTG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTGC
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCGTCTCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCCGG
601  CCGCGCGCCGT  TTTGCGCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGCATT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCTCCC  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgctGTTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCCTG  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCCCTG  TGCCGCCCTCA  TTCTGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCCG  TTTATATGCA
1251  CACATTGTTT  TGCTTgGCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTGAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPILLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLFSAATA ALLSRPSPF
101  SEILFSLDDA AAGIGLVLE LSFPIRFL LVLMEGRAL AFSSAQLVPK
151  LAILLLLPLT VGLLHFPANT SVLTAVYALA NLAAAFLF QNRCRLKAVR
201  RAPFSPAVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKKY AGLEQLGVYS
251  MGISFGGAAL LLOSIFSTVW TPYIFRAIEE NATPARLSAT AESAAALLAS
301  ALCLTGIFSP LASILLPENY AAVRFTVWSC MLPPLFYLT EISGIGLNVV
351  RKTRPIALAT LGALAANLLL LGLAVPSGGT RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAAAYLAG
451  CILRHRKLNH KLFHYLKKQG FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCCGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAC  CCTGTTCCTG  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTGC
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGCTCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTGCGCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGCATT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTG  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCCTG  TGCCGCCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCCG  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCTGTTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTGAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFTKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFELPIRFL LVLMEGRAL AFSSAQLVPK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*
```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA						
g717	10	20	30	40	50	60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA						
m717.pep	70	80	90	100	110	120
YVREYYATADKDTLFTKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE						
g717	70	80	90	100	110	120
YVREYYAADKDTLFTKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE						
m717.pep	130	140	150	160	170	180
LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTAVLTAVYALA						
g717	130	140	150	160	170	180
LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTSVLTAVALA						
m717.pep	190	200	210	220	230	240
NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY						
g717	190	200	210	220	230	240
NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY						
m717.pep	250	260	270	280	290	300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS						
g717	250	260	270	280	290	300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS						
m717.pep	310	320	330	340	350	360
ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT						
g717	310	320	330	340	350	360
ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT						
m717.pep	370	380	390	400	410	420
LGALANLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF						
g717	370	380	390	400	410	420
LGALANLLLGLAVPSGGTRGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF						
m717.pep	430	440	450	460	470	
CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX						
g717	430	440	450	460	470	
CLASSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKNLHKLHLYLKKQGFPLX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTTG CCGCCGCTGC
```

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTTCCAAG
451 CTGCCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCGGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGCTTAG AACAGCTCGG CGTTTATTTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCGCG
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCTTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTC GGTATTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCGTCTGCTG CTGGGGCTTG CCGTACCGTC CGCGGCGCGG CGCGGCGCGG
1151 CGGTTGCCCTG TGCCGCCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCTGCCGC TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGCGAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAAGTGTTC ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVSK
151 LAIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPLFLCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLGA
451 CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
a717.pep	YVREYYAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
m717	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIPLTVGLLHFPANTAVLTAVYALA
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIPLTVGLLHFPANTAVLTAVYALA
a717.pep	NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
m717	NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
a717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

1159

```

|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250       260       270       280       290       300
           310       320       330       340       350       360
a717.pep  ALCLTGIFSPLASLLL PENYA AAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||:|||||
m717      ALCLTGIFSPLASLLL PENYA AAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310       320       330       340       350       360
           370       380       390       400       410       420
a717.pep  LGALAANLLLLGLAVPSGGARGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
           |||||:|||||
m717      LGALAANLLLLGLAVPSGGARGAAVACAASFWLFFFAFKTESSCRLWQPLKRLPLYLHTLF
           370       380       390       400       410       420
           430       440       450       460       470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           430       440       450       460       470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTC TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGCGGCGCGG GCTGATTTTG GGGCAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTC AAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCGCGGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQRNG LFRTLWLYM FKHYAVHDFE EFLEYGMPI RIGKYGAGT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMAW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVQ
251 IPESWVRDKL VIPDVQEGEA VLVROVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILQDTHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CCGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCAACACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHFLFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRPVKF EFDTRPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

```

120      130      140      150      160      170
a718.pep  DSLPTLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLLRT
m718      |||||:|||||
          SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT
                        10      20      30

180      190      200      210      220      230
a718.pep  RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI
m718      |||||:|||||
          RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI
                        40      50      60      70      80      90

240      250      260      270      280      290
a718.pep  RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLOMADW
m718      |||||:|||||
          RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADW

```

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRDRLVSDAKVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTRPKDIAVFADAI PKLVDVGVIPIESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRVPKFEFDTRPKDIAVFADAI PKLVDVGVIPIESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	340	350	360	370	380	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTAACACTGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCT TTCGAGCGGT GCGGGAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAG TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAAC CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGRKRALLT LNWRVAPPRN
101 ATPEEKLSLD QAYEMMDSLP TLEDLINDLM DAVGHGFSAL EWEVWVSDGL
151 YLPRNFIHRP QSWFKWKDKN GLLLRITREN EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQMAWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCGGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGCGCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAATATCCC CATGCCGACC CAAACCGCGT
1101 CCGGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTGAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep
1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHLEFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHLEFADIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
m718-1	RAQHLEFADIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPNFIHRPQSWFKWDKDNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPNFIHRPQSWFKWDKDNGLLLRTRNP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPNFIHRPQSWFKWDKDNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPNFIHRPQSWFKWDKDNGLLLRTRNP					
	130	140	150	160	170	180

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVHTQKSRSVQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVHTQKSRSVQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMAWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMAWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRDDLVSADAKVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDDLVSADAKVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVI PESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVI PESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDPNPNVRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
m718-1	QVPDPNPNVRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCCGC	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGCGCG	GCAGCGGCAA	GGCATCACAA	AATGATTTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTTGGC	ACTTGAACCT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAA	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTTAGACGGC	ACTTTTCGAGG	TGCGGGATAT
801	GGTTCCGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCGG	CGGTTTGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCTGCG	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTCGCCTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTCGATT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCAG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAATATGCT	TAAGGGCGCG
1201	CTTTTGCGCG	AACTGCTGCC	TGATTTGCAG	GCAAAACAAG	GTTTGCTGCG
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGCGTGCGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTTGC GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CCGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pep

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIOR EIMLTQAAFN RLARSGKASQ NDLARAATVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPMADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAOTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSQSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNGK IAKNNEARML
451 SAAAQQEQQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLDGTLEPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQOQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVs RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CGGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTG TTTGATTG GCGGCTCGG CCAAGCTGTT
601 CGGGCGCGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TCGGATATA TCGGTCATGG TAGATACTGG CATAACCGCT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTGCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCGGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCTGCA AAACCGCCTG AACCAGTTAA

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGCGGTGGC AACGGCATT AATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTTGA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCAGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCC CGAGTTTAC GGCATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNKGA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNLRL NRLTAKQVQP VAQAVRLLST
301 SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGLLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPFIHHPA FIKRGTLVNS YAK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCGTGCAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGGCGGTC ATCAACCAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNLRLNLT AKQVQVPAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESELRRA
101 GRLNALVA AV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HIHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

m720.pep      250      260      270      280      290      300
SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
a720          |||||
              GLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
              10      20      30

m720.pep      310      320      330      340      350      360
SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720          |||||
              SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
              40      50      60      70      80      90

m720.pep      370      380      390      400      410      420
QTAESELRRAAGRLNALVA AVINQKPLIVRQAPIDGTIHQIAHEFYGDIA RAAELVRLNP
a720          |||||
              QTAESELRRAAGRLNALVA AVINQKPLIVRQAPIDGTIHQIAHEFYGDIA RAAELVRLNP
              100     110     120     130     140     150

m720.pep      430      440
HIHHPAFIKRGTLVNSYAKX

```

a720

|||||
HIHHPAFIKRGTLVNSYAKX
160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq

```
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGCGGCGAT TGTCCGCGCT CGTGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACTGGCA GGCTCGCAAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG
1001 CAAAAATGCT GGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA
```

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep

```
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHDTVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAQEQAD KGNELITAAL TSGKLLPAQK EWAKGVLPQK GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq

```
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGCGGCGAT TGTCCGCGCT CGTGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCGA
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACTGGCA GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG
1001 CAAAAATGCT GGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
```


1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

a721.pep
 1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
 151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV
 251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
 301 ENAQPVAAAL GSQTGGKAPD ERVAALTAE AAAAKMLGMS GEEFVKIKES
 351 EGK*

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
m721	10	20	30	40	50	60
a721.pep	70	80	90	100	110	120
m721	70	80	90	100	110	120
a721.pep	130	140	150	160	170	180
m721	130	140	150	160	170	180
a721.pep	190	200	210	220	230	240
m721	190	200	210	220	230	240
a721.pep	250	260	270	280	290	300
m721	250	260	270	280	290	300
a721.pep	310	320	330	340	350	
m721	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

m722.seq
 1 GTGTTTGAAG CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
 101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
 151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCCG ACCGCGAGTA
 201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCGC AATCCTACCA
 251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTCA
 301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCG
 351 CGCCGTTATC GGCAGCGGCG GCACGCGCGA AATACCGGCA ATCGCCGACG

```

401 AGCCGGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGTGC CCGGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGCGG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGTCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGTGC CCGGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1   ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC  CGTTTACAAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGCGAT  TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCGCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTTCAGCAT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGGCGG GTTTCTGGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1   MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAIIHAQLH
51  FAFGHSTQQV EHVDFVAHAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCGCTTTTTTTGCGGTGTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTTCGGGAAAAATCACGCTGGTGGTGTCTGCCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+ 120
GACGCGCGCGGAAAGCCCTTTTGTAGTGCAGCACACAGCAGGCTCGGCTATGTGCGG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTGATGGCGTAGTTTTTGGGAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTTAGCACTAATTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361 -----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGAGACCAGTGCAGTGTGACGGCGCAA
421 -----+-----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481 -----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAAATCG
a      G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541 -----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGGCCGCGCTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601 -----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCGTAGCCGCGCTTTTGAATGGCCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661 ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGCTTGCC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGACCGG GTTAAGTGA
401 AACAAACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501  CGGCATGGCC  GTCGAGGGCG  GCGACGGAGC  CACCTTTAGC  GGCGATGTTA
551  ACCAAACGGG  CGGCAGCTTT  AACACCGACG  GCGACGTGGT  GGCCGGCAAT
601  ATATCGTTGC  GCCAGCACCC  GCATACCGAC  AGCATCGGCG  GCAAAACCTT
651  ACCGGCGGAA  CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
  1  MSLSKLAKKT  AQTAKNIGET  LRAAFRGKIT  LVVSSEPIQR  VQLSGLADET
 51  LQDLEHLQEY  GFASHPPDGS  EAVVIPLGGN  TSHGVIVCSQ  HGSYRIKNLK
101  PGETAIFNHE  GAKIVIKQ GK  IIEADCDVYR  VNCKQYEVNA  ATDAKFNAFL
151  VETSAVLTAQ  GQINGNGGMA  VEGGDGATFS  GDVNQTGGSF  NTDGDVVAGN
201  ISLRQHPHTD  SIGGKTLPAE  PA*

```

a724/m724 100.0% identity in 222 aa overlap

a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
	10 20 30 40 50 60
a724.pep	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK
m724	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK
	70 80 90 100 110 120
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
	130 140 150 160 170 180
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
	190 200 210 220

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
  1  ATGGTGCGCA  CGGTTAAAG  CTACAACGGC  GAGGCCGACG  ATTTGGCGGG
 51  GCAAATCCAT  ACGCTGCCTG  CGGTTTGGGT  AACGTATGGC  GGCAGCAAAG
101  TTGAGCCTGC  CAGCACCGGC  GGCGTATGCG  GACGTTATCA  GGATACCGCC
151  GAATTTGTGG  TGATGGTGGC  GGCCCGCAAT  CTGCGCAACG  AGCAGGCGCA
201  GCGGCAAGGC  GGCATCGACA  GCCGCGAAAT  CGGCAGCAAC  GATTTAATCC
251  GCGCTGTTCC  CCGCTGCTT  GACGCGCAGC  GGCTCGGTTT  TGCCGATAGC
301  CGCGGCTTGG  TGCCCAAAGC  GGTGCGCGCG  ATTGCCAATC  ATGTGCTGGT
351  GCAAAACGCC  GCAGTAAGCA  TATATGCGGT  TGAGTATGCC  ATCCGCTTTA
401  ACACCTGCGG  GTTGGAAAT  GACCGCTACC  CCGAACGCAC  CGACAATCCC
451  GACGACCCCA  ACCATATCTT  TACCAAGTAT  CAGGGTACAT  TGAGCGAGCC
501  GTGGCCTGAT  TTCGAGGGGT  TGGACGGCAA  AATTTACGAC  CCGCAATCCG
551  CCGATGAAAT  ACCTGTAAAC  CTAACCCTTA  AGGATAAGCA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
  1  MVRTVKS YNG  EADDLAQI H  TLPVWVTY G  GSKVEPAST G  GVCGRYQDTA
 51  EFVVMVAARN  LRNEQAQRQG  GIDSREIGSN  DLIRAVRRL  DGQRLGFADS
101  RGLVPKAVRA  IANHVLVQNA  AVSIYAVEYA  IRFNTCGLEN  DRYPERTDNP
151  DDPNHIFTKY  QGTLSEPWPD  FEGLDGKIYD  PQSADEIPVN  LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

m726.seq

```

1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

m726.pep

```

1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

a726.seq

```

1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

a726.pep

```

1  MTIYFKNGFY DDTLGSIEPG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVVEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*

```

a726/m726 95.5% identity in 201 aa overlap

```

          10      20      30      40      50      60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726      MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          10      20      30      40      50      60

```

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGAAAAARFAEQKTATAFRLLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQLEDKLNIT
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              |||||:|:|:|||||:|||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq      not found yet
g727.pep      not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPPD SRNPNTGFRL FSPQIPNFT QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHLGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
m727      YARELELARAEEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDPSRNPTGTF
           70      80      90      100     110
a727.pep   IDGFGHHGLQLYKRALGYGNX
           120     130     140
m727      RLFSPQIPPNFTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGGT ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGGAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGGTTCG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC ATCATGCGC AACAGACGTG GTATTTGGAT GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKEKPVLL SFFALVEAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLOSEK DYLAIAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQ AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```



```

501  CGGGGAAAAT  TATGAAACGA  CAGGAGAATA  TCGGGTTGTT  TGGCAACCAG
551  ACGGTTTCGGT  ATTTGATGCG  GCGGGGCGCG  GGAAATCGG  GGAAGATGTT
601  TATGAGCATT  GCCTCGGGTG  TTATCAGATG  GCCCAGGTAT  ATTTGGCGAA
651  ATACCGGGAT  GTCGCGAATG  ACGAGCAGAA  GGTTTGGGAC  TTCCGCAAAG
701  AGAGCAACCG  AATTGCGTCG  GACTCGCGCA  ATTCTGTGTT  TTATCAGAAT
751  ATGCGGGAAT  TGATGCCCGG  AGGGATGAAG  GCGAACAGTC  TTGTGGTCGG
801  CTATGATCGG  GACGGTCTGC  CGCAAAAAGT  CTATTGGAGT  TTCGACAATG
851  GAAAAAACG  CCAGAGTTTC  GAATATTATT  TGAAAAACGG  AAATCTTTT
901  ATTGCACAAT  CTTGACGGT  AGCATTGAAA  GCGGATGGCG  TAACGGCGGA
951  TATGCAGACC  TATCATGCGC  AACAGACGTG  GTATTTGGAT  GCGGGCGGA
1001 TTGTCCGCGA  AGAGAAACAG  GGAGACAGAC  TGCCTGATT  TCCTTTGAAC
1051 TTGGAAAATT  TGGAAAAAGA  GGTGCGCCGT  TATGCAGAGG  CTGCGGCGAG
1101 ACGTTCGGGC  GGCAGGCGCG  ACCTTTCTCA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1  MFKKFKPVLL  SFFALVFAFW  LGTGIAYEIN  PRWFLSDTAT  EVPKNPNAFV
51  AKLARLFRNA  DRAVVIVKES  IRTEENLAGT  VDDGPLQSEK  DYLAALAIRLS
101 RLKEKAKWFH  VTEQEHGKEV  WLDYHIGEGG  LVAVSLSQRS  PEAFVNAEYL
151 YRNDRPFSVN  VYGGTVHGEN  YETTGEYRVV  WQPDGSVFDA  AGRGKIGEDV
201 YEHCLGICYQ  AQVYLAKYRD  VANDEQKVWD  FRKESNRIAS  DSRNSVFYQN
251 MRELMPRGMK  ANSLVVGYDA  DGLPQKVYWS  FDNGKKRQSF  EYYLKNGNLF
301 IAQSSTVALK  ADGVTADMQT  YHAQQTWYLD  GGRIVREEKQ  GDRLPDFPLN
351 LENLEKEVRR  YAEAAARRSG  GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
	: : : : :					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	: : : : :					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
	: : : : :					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKNESNRIAS					
	: : : : :					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVFYQNMRELMPRGMKANSLVVGADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	: : : : :					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	: : : : :					

```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310           320           330           340           350           360
m728.pep  YAEAAARRSGGRRDLSHX
           |||||
g728      YAEAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAAG TCTATTGGAG TTTGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCGCG
1001 AAGAGAAACA GGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGCGAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLERNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLVRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDR DSVFYQNMRE
251 LMPRGMKANS LRVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

a728 / m728    96.3% identity in 377 aa overlap

           10           20           30           40           50
a728.pep  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10           20           30           40           50           60

           60           70           80           90           100          110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70           80           90           100          110          120

           120          130          140          150          160          170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLVRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLVRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130          140          150          160          170          180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGVSFSDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGVSFSDAAGRKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSILVVGYDADGLPQKVYWSFDNGKKRQSFYYLKNLNF					
m728	DSRNSVFYQNMRELMPRGMKANSILVVGYDADGLPQKVYWSFDNGKKRQSFYYLKNLNF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGRRDLSHX					
m728	YAEAAARRSGRRDLSHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA  CATTGAAAC  TACCTTGACC  TCTGTTGCAG  CAGCCTTTGC
51  ATTGTCTGCC  TGCACCATGA  TTCCTCAATA  CGAGCAGCCC  AAAGTCGAAG
101  TTGCGGAAAC  CTTCCAAAAC  GACACATCGG  TTTCTTCCAT  CCGCGCGGTT
151  GATTTGGGTT  GGCATGACTA  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201  CGACATCGCA  CTCGAGCGCA  ATACCAGTTT  GCGTACAGCC  GTATTGAACA
251  GCGAAATCTA  CCGCAAACAA  TACATGATCG  AGCGCAACAA  CCTCTGCCCC
301  ACGCTTGCCG  CCAATGCGAA  CGGCTCGCGC  CAAGGCAGCT  TGAGCGGCgg
351  caaTGTCAGC  AGCAGCTACA  ATGTCGGAAT  GGGTGcGGca  tCTTACGAAC
401  TCGATCTGTT  CgGGCGCGTG  CGCagcaaca  GcgaagcAGC  ACTGcaggGC
451  tATTTTGCCA  GCGTTGCCAA  CcgCGATGCG  GCACATTTGa  ttCtGATTGC
501  CACCGTTGCC  AAAGCCTATT  TCAAcgaGcG  TTATGCCGAA  AAAGcgatgT
551  CTTTGCGCGCa  gcGTGTCTTG  AAAACGCGCG  AGGAAACCTA  CAAGCTGTCC
601  GAATTGCGGT  ACAAGGCAGG  CGTGATTTCC  GCCGTGCCCC  TGCGCCAGCA
651  GGAAGCCTTG  ATTGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCa
701  gcCGCGAACA  GGCGCGCAAT  GCCTTGCGAA  CCTTGATTAA  ccGTCCGATA
751  CCCGAagaCC  TGCCCGCCGG  TTTGCCGTTG  GACAagcAGT  TTTTGTGTGA
801  AAAACTGCGT  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCGACA
851  TCCGCGCCGC  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901  gcgCGCGCCg  ccTTTTTCCC  GTCCATCCGC  CTGACCGGAA  GCGTCGGTAC
951  GGGTTCTGTC  GAATTGGGCG  GGCTGTTCAA  AAGCGGCACG  GGCGTTTGGG
1001  CGTTCGCTCC  GTCTATTACC  CTGCCGATTT  TTAATTGGGG  AACGAACAAG
1051  GCGAACCTTG  ATGTGGCAAA  ACTGCGCCAA  CAGGCACAAA  TTGTTGCCTA
1101  TGAATCCGCC  GTCCAATCCG  CCTTTCAAGA  CGTGGCAAA  GCATTGGCGG
1151  CGCGCGAGCA  GCTGGATAAA  GCCTATGACG  CTTTAAGCAA  ACAAAGCCGC
1201  GCCTCTAAAG  AAGCGTTGCG  CTTGGTCGGA  CTGCGTTACA  AACACGGCGT
1251  ATCCGGCGCG  CTCGATTTGC  TCGATGCGGA  ACGCATCAGC  TATTGGGCGG
1301  AAGGTGCGGC  TTTGTGCGCA  CAACTGACCC  GCGCCGAAAA  CCTTGCCGAT
1351  TTGTACAAGG  CGCTCgacGG  CGGATTGAAA  CGGGATACCC  AAACCGGCAA
1401  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTLT  SVAAAFALSA  CTMIPQYEQP  KVEVAETFQN  DTSVSSIRAV
51  DLGWHDYFAD  PRLQKLIDIA  LERNLSLRTA  VLNSEIYRKQ  YMIERNLLP
101  TLAANANGSR  QGSLSGGNVS  SSYNVGLGAA  SYELDLFGRV  RSNSEAALQG
151  YFASVANRDA  AHLILIATVA  KAYFNERYAE  KAMSLAQRVL  KTREETYKLS

```

m729.seq

m729.pcp

BNSDOCID: <WO__9957280A2_1_>

1179

m729.pep	70	80	90	100	110	120
	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
m729.pep	130	140	150	160	170	180
	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
g729	SSYNVLGAASYELDLFGRVRSNSEALQGYFASVANRDAAHLLIATVAKAYFNERYAE					
	130	140	150	160	170	180
m729.pep	190	200	210	220	230	240
	EAMSLAQRVLKTRRETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
g729	KAMSLAQRVLKTRRETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
	190	200	210	220	230	240
m729.pep	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
m729.pep	310	320	330	340	350	360
	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGSGVTGSVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
m729.pep	370	380	390	400	410	420
	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420
m729.pep	430	440	450	460		
	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTCGC
51	ATTATCCGCC	TGCACCATGA	TTCCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACCGCCG	ACAGCGGCAT	CCGTGCGGTC
151	GATTTGGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAAGTT	GCGTACCGCC	GTATTGAACA
251	GCGAAATCTA	CCGCAAAACAA	TACATGATTG	AGCGCAACAA	CCTCCTGCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	TCTTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTGCAAGGC
451	TATTTCCGCA	GCACCGCCAA	CCGCGATGCG	GCACATTGTA	GCCTGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAACGAACG	TTATGCCGAA	GAAGCGATTGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTC	GCCGTCGCCC	TACGTCAGCA
651	GGAAGCCCTA	ATCGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	GCCTTGGA	CCCTGATTAA	CCAACCGATA
751	CCCGACGACC	TGCCCGCCGG	TTTGCCGTTG	GACAAGCAGT	TTTTTGTGTA
801	GAAGCTGCCG	GCCGGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCCG	CCTTTTTC	ATCCATCCGC	CTGACCGGAA	GCGTCGATAC
951	GCATTCTGCC	GAATTGGGCG	GGCTGTTCAA	AAGCGGCACC	GGCGTTTGGT
1001	TGTTTCGACC	TTCCATTACC	CTGCCGATTT	TTACCTGGGG	TACGAACAAG

1180

```
1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```
1 MDTTLKTTLT SVAAAFALSA CTMIPQYEOP KVEVAETFKN DTADSGIRAV
51 DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEAAALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*
```

a729 / m729 98.1% identity in 467 aa overlap

```
          10          20          30          40          50          60
a729.pep  MDTTLKTTLT SVAAAFALSA CTMIPQYEOP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          |||
m729       MDTTLKTTLT SVAAAFALSA CTMIPQYEOP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          10          20          30          40          50          60

          70          80          90          100         110         120
a729.pep  PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP TLAANANDSR QGSLSGGNVS
          |||
m729       PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP TLAANANDSR QGSLSGGNVS
          70          80          90          100         110         120

          130         140         150         160         170         180
a729.pep  SSKVGLGAAS YELDLFGRV RSSSEAAALQGY FASTANRDA AHLSLIATVA KAYFNERYAE
          |||
m729       SSKVGLGAAS YELDLFGRV RSSSEAAALQGY FASTANRDA AHLSLIATVA KAYFNERYAE
          130         140         150         160         170         180

          190         200         210         220         230         240
a729.pep  EAMSLAQRVL KTREETYKL SELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
          |||
m729       EAMSLAQRVL KTREETYKL SELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
          190         200         210         220         230         240

          250         260         270         280         290         300
a729.pep  ALATLINQPI PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
          |||
m729       ALATLINQPI PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
          250         260         270         280         290         300

          310         320         330         340         350         360
a729.pep  ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ
          |||
m729       ARAAFFPSIR LTGTGTGSA ELGGLFKSGT GVWSFAPSIT LPIFTWGTNK ANLDVAKLRQ
          310         320         330         340         350         360

          370         380         390         400         410         420
a729.pep  QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVG LRYKHGVSGA
          |||
m729       QVQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR ASKEALRLVG LRYKHGVSGA
          370         380         390         400         410         420
```

	430	440	450	460
a729.pep	LDLLDAERSSSYSAEGAALSAQLTRAENLADLYKALGGGLKRD	TQTDKX		
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRD	TQTDKX		
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1   GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGTTCGA CTCATACAGC CCGCCCTCGC GCGGGAATTG GCGCAAGACC
101 CGTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGcgaCCC GCGCGGCAGC GTTCCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCGGC AATCCAAGGC AATCTTGTTT ACACCGTCCG CTTTTCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GCGGCAATT ACCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCGCA
551 GCATCCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCAACGGC GTCGCCCGCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCGA TGCGCAACAT
801 CGCCCCCTTA CCCGCGGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAGAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGCGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAAACCCGT TACCGCCCGA TACGGCAATC CGTATCAAGA AACCCTTAC
1201 ATTGAAGTTT CAGACGGCAT CGGCAACAGC CAAACCCTGA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGGCAAATG GATTAAGGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAA ACCGCTCAA GCCTACAATC TGACCGTTGC
1401 GATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAATGATTGT CCGCCTAAAC CAAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTTCGG AAGGAAAGCA ATATTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAAG
1701 GGTAAAAAAT GGGAAATGGA CACCAAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1   VKPLRRLTNL LAACAVAAVA LIQPALAADL AQDPFITDNT QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGH LLIQQAIIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDDGFTV YRLNWEHGH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIF DNYNNLGSNF
201 SDRADANRK MFEHNAKLDR WGNSEFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKF AAG IGLGSAAGFEK NTREAVDRWI
301 QENPNAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTDAGY KAIAHIQAGD RVLKDEASG ETGYKPVTA YGNFYQETVY
401 IEVSDGIGNS QTLISNRIHP FYSKGWIKI EDLKAGSRL SESGKTQTVR
451 NIVVKPKPLK AYNLTVDWH TYFVKGNQAE TEGVWVHND PPKPKPTNHA
501 QQRKEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTPD
551 GRQVTQFKNS KANTSKRVKN GKWTFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1   GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGGCGCGCA CTCATACAGC CCGCCCTCGC GCGGGAATTG GCGCAAGACC

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1182

```
101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GCGCGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

m730.pep

```
1 VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQORIS DNYSNLGSNF
201 SDRADANRKF MFEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFNLQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*
```

g730 / m730 93.0% identity in 344 aa overlap

```
10 20 30 40 50 60
g730.pep VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730 VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
10 20 30 40 50 60

70 80 90 100 110 120
g730.pep VSDRTGKINVIQDYTHQMGNLLIQQAIIQGNLGYTVRFSHGHEEHAPFDNHAADSASEE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730 VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
70 80 90 100 110 120

130 140 150 160 170 180
g730.pep KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730 KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT
130 140 150 160 170 180

190 200 210 220 230 240
g730.pep DTRSIRQORIFDNYNNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730 DTRSIRQORISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI
190 200 210 220 230 240
```


	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAAPGKAAVSGDFSKSYTCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVTRYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GCGCGCCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCGCAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTTCG  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACTAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACGT
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRLRIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADANRKA  MFEHNAKLDR  WGNMSEFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAKAA  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPKG  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

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a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNHINVLSGNSIQHILYGEAGGGHLFPKPGKTTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRKKTGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gatttttcgag  cgtttttcatg  CGAGAACGGT  TTGTCTGTGC  GCGTCCGCAA
51  TTTGGACGGC  GGCAAAATCG  CGTTGCGGCT  GGACGGCAGG  CGTGCCGTCC
101 TCTCTTCCGA  CGTTGCCGCA  TCCGGCGAAC  GCTATACCGC  CGAACACGGT
151 TTGTTTCGAA  ACGGAACCGA  GTGGCACCAG  AAAGGCGGCG  AAGCCTTTTT
201 CGGCTTTACC  GATGCCTACG  GCAATTCGGT  CGAAACTTCC  TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG  LSVRVRNLDG  GKIALRLDGR  RAVLSSDVAA  SGERYTAEHG
51  LFGNGTEWHQ  KGGEAFFGFT  DAYGNSVETS  CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGACGCGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCGGC  ACGGACGATT  TTCGGGCGTT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCGCGT  CCGCCATTG  GACAGCGGCA  AAGTCGCGTT
201 GCGGCTGGAC  GGCAGGCGTG  CCGTCCTCTC  TTCCGACGTT  GCCGCATCCG

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251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

g731.pep					10	20	30
					DFRAFSCENGLSVRVRNLDGGKIALRLDGR		
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHLDSGKVALRLDGR						
	20	30	40	50	60	70	
g731.pep		40	50	60	70	80	
		RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX					
m731		RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX					
		80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCCG
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTT GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

a731.pep		10	20	30	40	50	60
		MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTAD	DFRAFSCENGLSVHVRRL			
m731		MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHL				
		10	20	30	40	50	60
a731.pep		70	80	90	100	110	120
		DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE					
m731		DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE					
		70	80	90	100	110	120

a731.pep TSCRARX
 |||||
 m731 TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtC CTGCCGGTGC AATCCATCCG TACGATGGCG

```

151 GAGGTTTACG GTCAGATTAA GGCAAACACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTGCGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTACAG ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGgtattGG TcaaTTCGGG
951 TTCggcttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTGAGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAG AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGCGACCTG
1201 TCGGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGCG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732 . pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGF A EKDGRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDG MVLKAVPEDYV YGMGGDPLAG
301 IPAEKLTIPM TVLVNSGSAS ASEIVAGALQ DHKRAIVGT QSFGKGSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732 . seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTACAG ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCATTCTCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GCGCGATTGT
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAEKLTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLNSGSAV KLTALYYTTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
g732	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSSEFGGLGMEIGQEDGFVKV					
g732	70	80	90	100	110	120
	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSSEFGGLGMEIGQEDGFVKV					
m732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	130	140	150	160	170	180
	VSPIEDTPAERAEVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS TKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS TKGRDGKDMVLKAVPEDYVYGMGGDFLAG					
m732.pep	310	320	330	340	350	360
	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
g732	310	320	330	340	350	360
	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKKDKKX					
g732	PVSNDKKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

a732.seq

1	ATGTCGAAAC	CTGTTTTTAA	GAAAATCGCA	CTTTATACTT	TGGGTGCAAT
51	CAGCGGCGTG	GCCGTCAGTC	TGGCGGTGCA	GGGTTTGGCC	GCCGAGAAGG
101	ACAGGCGGGA	TAACGAAGTC	CTGCCGGTGC	AATCCATCCG	CACAATGGCG
151	GAGGTTTACG	GTCAAATCAA	GGCAAACACTAC	TATCAGGACA	AACCCGATGC
201	CGATTTGTTT	GAAGGTGCGA	TGAAGGGTAT	GGTGGCCGGT	TTGGATCCGC
251	ATTCCGAATA	TATGGATAAA	AAAGGTTATG	CCGAGATAAA	GGAGTCCACC
301	AGCGGCGAAT	TTGGCGGCTT	GGGGATGGAA	ATCGGGCAGG	AAGACGGATT
351	TGTCAAAGTG	GTTTCGCCGA	TTGAGGACAC	GCCTGCGGAA	CGGGCGGGGG
401	TGAAAAGCGG	CGATTTTCATT	GTGAAAATCG	ATAATGTTTC	GACACGCGGC
451	ATGACGCTCA	GCGAAGCGGT	GAAGAAAATG	CGGGGCAAGC	CGGGTACGAA
501	GATTACTTTG	ACGCTGTCCG	GCAAAAATGC	CGACAAGCCG	ATAGTCGTCA
551	ACCTGACCCG	TGCCATTATT	AAAGTGAAAA	GCGTCCGCCA	TCACCTGATC
601	GAACCCGATT	ACGGCTATAT	CCGCGTGTCTG	CAGTTCCAAG	AGCGGACGGT
651	CGAAAGCGTC	AATACCGCCG	CAAAAGAGCT	GGTAAAGGAA	AATAAAGGAA
701	AACCGCTCAA	GGGGCTGGTG	TTGGATTTCG	GCGACGACCC	CGGCGGGCTT
751	TTGACTGGCG	CGGTGCGCGT	GTCGGCGGCA	TTTCTGCCGT	CTGAAGCAGT
801	CGTCGTCAGC	ACCAAGGGAC	GCGACGGCAA	AGACCGCATG	GTAAGGAAAG
851	CCGTTCTCTGA	AGATTATGTG	TACGGGATGG	GCGGCGATTG	GTTGGCGGGC
901	ATTCTGCGG	AGTTGAAAAC	CATACCGATG	ACGGTATTGG	TCAATTCCGG
951	TTCGGCTTCC	GCGTCGGAGA	TTGTCGCAGG	TGCATTGCAG	GATCATAAAC
1001	GCGCGGTCAT	CGTCGGTACG	CAGAGCTTCG	GCAAAGGTTT	GGTTCAGACT
1051	TTGATTCCCTT	TGTCCAACGG	CAGCGCGGTC	AAGCTGACAA	CGGCACTGTA
1101	TTATACGCCG	AACGACCGTT	CTATTTCAGG	GCAGGGGATT	GTTCCCGATG
1151	TCGAAGTAAA	AGATAAGGAA	CGCATTTTGT	AAAGCCGCGA	GGCGGATTTG
1201	GTCGGACACA	TCGGCAATCC	TTTGGGCGGC	GAGGATGTGA	ACAGTGAAC
1251	CCTTGCCGTG	CCGCTTGAAA	AAGATGCGGA	TAAGCCCGCT	GTAAGAGAAA
1301	AAGGTAAAAA	GAAAAAGGAC	GAGGATTTGT	CTTCAAGGCG	GATTCCCAAC
1351	CCTGCCAAAG	ACGACCAAGT	GCGGAAAGCT	TTGGATTTAG	TCAAGTCGCC
1401	CGAGCAGTGG	CAGAAGTCTT	TGGGGCTGGC	GGCGAAAAAG	CCGGTTTCAA
1451	ATAAAGATAA	GAAAGATAAA	AAAGATAAGA	AGTAG	

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

a732.pep

1	MSKPVFKKIA	LYTLGAISGV	AVSLAVQGFA	AEKDRRDNEV	LPVQSIRTMA
51	EVYGOIKANY	YQDKPDADLF	EGAMKGMVAG	LDPHSEYMDK	KGYAEIKEST
101	SGEFGGLGME	IGQEDGFVKV	VSPIEDTPAE	RAGVKSDFI	VKIDNVSTRG
151	MTVSEAVKKM	RGKPGTKITL	TLSRKNADKP	IVVNLTRALI	KVKSVRHHLI
201	EPDYGYIRVS	QFQERTVESV	NTAAKELVKE	NKGKPLKGLV	LDLRDDPGGL
251	LTGAVGVSA	FLPSEAVVVS	TKGRDGKDRM	VLKAVPEDYV	YGMGGDSLGA
301	IPAEELKTIPM	TVLVNNGSAS	ASEIVAGALQ	DHKRAVIVGT	QSFGKGSVQT
351	LIPLSNGSAV	KLTTALYYTP	NDRSIQAQGI	VPDVEVKDKE	RIFESREADL
401	VGHIGNPLGG	EDVNSETLAV	PLEKDADKPA	VKEKGKKKKD	EDLSSRRIPN
451	PAKDDQLRKA	LDLVKSPEQW	QKSLGLAAKK	PVSNDKKDKK	KDKK*

a732/m732 99.6% identity in 494 aa overlap

a732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPVQSIRTMAEVYGGQIKANY					
m732	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPVQSIRTMAEVYGGQIKANY					
a732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGGLGMEIGQEDGFVKV					
m732	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGGLGMEIGQEDGFVKV					
a732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
a732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
a732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
m732	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
a732.pep	310	320	330	340	350	360
	IPAEKLTIPMTVLVNSGSASASEIVAGALQDCHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	310	320	330	340	350	360
	IPAEKLTIPMTVLVNSGSASASEIVAGALQDCHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
a732.pep	370	380	390	400	410	420
	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	370	380	390	400	410	420
	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
a732.pep	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
a732.pep	490					
	PVSNKDKKDKKDKKX					
m732	490					
	PVSNKDKKDKKDKKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

1	ATGATGAATC	CGAAAACTT	GGGCCGTTT	TCGCTGTGT	CGGCGGTCT
51	GGCTCTGACC	GCCTGCGCCG	GCGGCGGGCA	TAAAAACCTG	TATTATTACG
101	GCGGTTATCC	CGATACCGTC	TATGAAGGTT	TGAAAAACGa	cgACACTTCG
151	TTGGGCAAGC	AGACCGAAAA	GATGGAAAAA	TACTTTGCGG	AAGCCGCCAA
201	CAAAAAATG	AATGCCGCC	CGGGTGC	CGCCATTG	GGACTGCTGC

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251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPCTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

m733.pep	10	20	30	40	50	60
	MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	: : : : : :					
g733	10	20	30	40	50	60
	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	: : : : : :					
g733	70	80	90	100	110	120
	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

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1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

a733/m733 100.0% identity in 123 aa overlap

	10	20	30	40	50	60
a733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
m733	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	GKRX					
m733	GKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

g734.seq
 1 ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
 51 GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
 101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
 151 AAAAGCGAAG CGTTTGCCGA GTTGGAAAGCC TTTTGCAAAG GTCAGGACAC
 201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
 251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
 301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
 351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
 401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGCGCGG
 451 GCTGTTTCGCT CCTTAATCCA ACACCTGAAA TAA

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

g734.pep
 1 MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
 51 KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
 101 MRVENAVVIT SPRFTSVHQQ ALNQCIKKYG AQQCGLQTV YCTSSSYGG
 151 AVRSLIQHLK *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

m734.seq (partial)
 1 TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTCGCT
 51 GAACAATACC TGTGTCGCGC TGGCATAACC GAAAGCCTTG GCGCGCTGC
 101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTTAC GAGCGTTCAT
 151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
 201 CGGCTTGGA ACAGTGTATT GCACATCTTC TTCTTATTAC GCGGAACTG
 251 TCGCTCTTT GATTCAAAAT CTCAAATAA

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

m734.pep (partial)
 1 SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVDNAV VITS PRFTSVH
 51 QVALNQCIKK YGVQGCGL ETVYCTSSSY GGTVRS LIQN LK*

m734/g734 92.4% identity in 92 aa overlap

	10	20	30
m734.pep	SGIAEDEPTGCRSVSVLNNTCVALAYPKAL		
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVSVLNNTCVSLAYPKAL		

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	40	50	60	70	80	90
m734.pep	GALRVDNAVVITSPRFTSVHQVALNQCICKYGVQGQCGLETVYCTSSSYYGGTVRSLIQN					
g734	: :					
	100	110	120	130	140	150
m734.pep	LKX					
g734	LKX					
	160					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2497>:

```

a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTGT CAGGTTAAAA CCACAAAAGA AGATTCGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGACT TTCTGCAAG GT CAGGACAG
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCTGT
251 CGTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACAGATG TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIQNLK	*			

a734/g734 95.6% identity in 160 aa overlap

```

      10      20      30      40      50      60
a734.pep MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g734      MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA
          10      20      30      40      50      60

      70      80      90      100     110     120
a734.pep FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVLAYPKALGAMRVENAVVITSPRFTSVYQV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g734      FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV
          70      80      90      100     110     120

      130     140     150     160
a734.pep ALNQCIKKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g734      ALNQCIKKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLKX
          130     140     150     160

```

```
g735.seq    not found yet
g735.pep    not found yet
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2499>:

m735.seq

```
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTCG GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGGTCAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGCGCGAC GCTGTGCGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA CCGGTCTGAA ACGGAAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAAGCGG
```

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351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGCGC AAATCCGGCA
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GGCGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTTCGTCC GCCCTGACGA TTTTGCGCGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDING
 201 LIKSAAFGVA VTLLIAVHGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCCG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCCTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCCG GTGGTTGCCC CGCGTTTTTG GCGGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTTCGTCC GCCCTGACGA TTTTGCGCGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDING
 201 LIKSAAFGVA VTLLIAVHGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	: : : :					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	: : : :					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLWGLDS					
	: : :					
g736	MKTTGQLEAMNVMAVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTCCGT	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA
101	CGGCTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTCGG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTG	TCCGCATGGT
201	CTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAAATTCAAA	TCCGCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTAAACCC	CGTCGCCCGA	GTGGTTGCGC	CGCGCTTTTG	GGCGGGCGTG
451	TTTTCCATGC	CGCTTTTGCC	TTTCGATTTT	AACGTGGCGG	GTATTTTCGG
501	CGCGTATTTG	GTCGGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT
551	GGTCGCAAAT	GCAGAACAA	ATCACGATAC	ATTACGATGT	AATCAACGGT
601	CTGATCAAAT	CCGCCGCGTT	CGCGGTGGCG	GTAACGCTGA	TTGCCGTGCA
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTGGCGGGT	CGATTTTATA
751	TTGACCGCGT	GGATGTTTAC	AGATTGA		

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNLA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NVMAVNPVAR	VVAPRFWAGV
151	FSPMLLASIF	NVAGIFGAYL	VGVTWLGLDS	GIFWSQMNN	ITIHVDVING
201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGIL	RASTRTVVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
m736	MKTTEQLEAMNVMVAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

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m736      GIFWSQMONNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240
a736.pep  250      259
           ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq.

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR AQAEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737      MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR AQAEKAAWAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737      VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

a737.seq
1 ATGAACCTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep
1 MNFKRLLLTAAATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAHQHSKQDKIISRAQAEKAALAR					
	10	20	30	40	50	60
m737	MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX					
	10	20	30	40	50	60
m737	VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq
1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACCTGCC
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCGCGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAACA TCATCGTTCA
501 CAGAGGGCAA GGCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCCTCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATAA CGACAACCTT CTCAGCACCT TGTTACCCA TTCCCACAAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTCG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC AACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTAC TCCGCCACCT

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACAA
1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLFLA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHGW N SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQGVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAAC TGCC
51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGCCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGCGGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTACGCG CGTGGGCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCCG AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTACCCCA TTCCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m738.pep	MPAETT	VS	GAHPAAKLPIYILPCFLWIGIVPFTFALKLKPS	PDFYHDA	AAAAAGLIVLLFL	
g738	MSAETT	VS	GARPAAKLPIYILPCFLWIGIIPFTFALRLKPS	PDFYHDA	AAAAAGLIVLLFL	
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKL	FDVKIP	AI	SFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSI		
g738	TAGKKL	FDVKIP	AI	SFLLFAMAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL		
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQ	ERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN				
g738	VAHYGQ	ERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTP	LLQNIIVHRGQGVIGHIGQRN			
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMW	GILAAAYLNGQRKIP	AALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW			
g738	NLGHYLMW	GILASAYLNGQRKIP	AALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW			
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDK	SNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI				
g738	YFRSDK	SNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANGGFTDLPRQS				
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALA	AFQSAPIFGHGWNSFAQQTFLINAEQHNIYDNLLSNLFTHSHNIVLQLLAEMG				
g738	EWNKALA	AFQSAPIFGHGWNSFAQQTFLINAEQHTIHDNFLSTLFTSHSHNIILQLLAEMG				
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTL	LVAAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWVYVFLIPFGLML				
g738	ISGTL	LVAAATLLTGIAGLLKRSLTPASLFLLCALAVSMCHSMLEYPLWVYVFLIPFGLML				
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPA	EASDGI	AFKKAANLGILTASAAIFAGLLHLDWYTYTRLVNAFSPATDDSAKT	LN	NRK	
g738	FLSPA	EASDGI	AFKKAANLGILTASAAIFAGLLHLDWYTYTRLVNSFPAADDSAKTI	NRK		

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPLMSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPLMSFYADFSLVNFALPEYPETQTWAEATLKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

a738.seq

```

1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCGGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTTCCCT ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GGCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCAACCA TTCCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

a738.pep

```

1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAD
51  AAGLIVLLEF TAGKKLFDVK IPPISFLLFA MAAFYQLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYQERIV TFAWSLLIG SLLQSCIIVI
151 QFAGWEDTPL FQNIIVYSQGV VIGHIGQRN NLGHYLMWGI LAAAYLNGQR

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1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWRKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQNIHDNL LSNLFTSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAAEK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAH	PAAKLP	IIYILPC	FLWIGIV	PFTFALR	LQSPDFYH
m738	MPAETTVSGAH	PAAKLP	IIYILPC	FLWIGIV	PFTFALR	LQSPDFYH
	70	80	90	100	110	120
a738.pep	TAGKKLFDV	KIPPI	SFLLF	FAMAA	FWYLQ	ARLMNLI
m738	TAGKKLFDV	KIPPI	SFLLF	FAMAA	FWYLQ	ARLMNLI
	130	140	150	160	170	180
a738.pep	VAHYGQER	IVTLF	AWSL	LIGS	LLQSC	IVVIQF
m738	VAHYGQER	IVTLF	AWSL	LIGS	LLQSC	IVVIQF
	190	200	210	220	230	240
a738.pep	NLGHYLM	WGIL	AAAY	LNGQ	RKIP	PALGAIC
m738	NLGHYLM	WGIL	AAAY	LNGQ	RKIP	PALGAIC
	250	260	270	280	290	300
a738.pep	YFRSDK	SNRR	TILG	IAAA	VFLT	ALFQFS
m738	YFRSDK	SNRR	TILG	IAAA	VFLT	ALFQFS
	310	320	330	340	350	360
a738.pep	EWRKAL	AAFQ	SAPI	FGH	WNS	SFAQQT
m738	EWRKAL	AAFQ	SAPI	FGH	WNS	SFAQQT
	370	380	390	400	410	420
a738.pep	ISGTLL	VAAT	LLT	GIAG	LLK	RPLTP
m738	ISGTLL	VAAT	LLT	GIAG	LLK	RPLTP
	430	440	450	460	470	480
a738.pep	FLSPA	EASD	GIAF	KKAN	LGIL	TASAA
m738	FLSPA	EASD	GIAF	KKAN	LGIL	TASAA
	490	500	510	520	530	540
a738.pep	INELRY	ISAN	SPML	SFYA	DFSL	VNFAL
m738	INELRY	ISAN	SPML	SFYA	DFSL	VNFAL

1202

	550	560	570	580	590	600
a738.pep	MRQ	GKVAEAKQWM	RATQSYYPYLM	PRYADEIRKLPV	WAPLLPELLKDC	KAFAAAPGHPEA
m738	MRQ	GKVAEAKQWM	RATQSYYPYLM	PRYADEIRKLPV	WAPLLPELLKDC	KAFAAAPGHPEA
	550	560	570	580	590	600
a738.pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGG C G ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAAC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAA PKETPKKET PKENHTKPD T PKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGG C G ACAAACCCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAAC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCCCGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAA PKETPKENHT KPDPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPHKEILDKLF					
g739	PKNTPAKPHKEILDNLFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  POHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRQPDAGA Q AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLFX*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPOHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSPAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

              190
a739.pep      PKNTPPKPHKEILDNLFX
              |||||:|
m739          PKNTPPKPHKEILDKLF
              180   190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gTTTGTATT
201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTGT CTGTTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFTIKHH LKQFDLKRQ TMFLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAATCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTGTATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK FVLFDTIKHH
              |||||:|
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK FVLFTIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQFDLKRQ TMLLFIPII LLVYLFHYFG AFX
              ||| |||||:|:|:|:|:|:|
g740          LKQFDLKRQ TMLFIPIV LLVYLFHYFG AFX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```

```

a740.pep      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
|||||:|||||
m740          MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
|||||:|||||
m740          LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAA AACTTTCAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCTCCGCCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QORRGGGGGV AADIGTGLAD ALTAPLDCHKD
51  KGLKSLTLEA SIPQGTILT SAQGAETFK AGGKDNSLNT GKLNKDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHSA VVALRIEKIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCACAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTGCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDCHKDKGL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFTQ EQIQDSEHSG KMVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQNGNKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEGKS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---	ALILTACSSGGGGVAAD	IGAGLADALTAPLDHKDKGLQSLTLDQ		
g741	VNRTTFCCLSLTAGPDS	DRLQRRGGGGVAAD	IGTGLADALTAPLDHKDKGLKSLTLEA		
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAAQGA	EKTY---GNGDS	SLNTGKLKNDKVS	RFDFIRQIEVDG	QQLITLESGE
g741	SIPQNGTLTLSAQGA	EKTFKAGGK	DNLSLNTGKLKNDK	ISRDFVQKIEVDG	QTITLASGE
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQ	TEQIQDSEHSG	KMVAKRQFRIG	DIAGEHTSFD	DKLPEGGRATY
g741	FQIYKQDHS	AVVALRIE	KINNPDKID	SLINQSRFLV	SDLGGEHTAF
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYT	IDFAAKQNGNKIE	HLKSPELNVDL	AAADIKPDG	KRHAVISGS
g741	AFSSDDADGKLTYT	IDFAAKQGHGK	IEHLKTPEQ	NVELASAE	LKADEKSHAV
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGG	KAQEVAGSAE	VKTVNGIRHIG	LAAKQX	
g741	GEEKGTYRLALFG	DRAQEIAGS	ATVKIGEKV	HEIGIADKQX	
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTTCT	TTGACCGCCG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCCGCCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCGTCAGG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGCGGAAA	AAACTTATGG	AAACGGCGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTCGGA	GCATTACAGG	AAGATGGTTG	CGAAACGCCA	GTTCAGAATC
451	GGCGATATAG	CGGGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCCG	TTCAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTCCGCCGCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTTGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCTTTACA
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	GCCGCCAAGC	AGTAA		

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAAQ	GAEKTYGNGD	SLNTGKLKND	KVSRFDFIRQ
101	IEVDGQLITL	ESGEFQVYKQ	SHSALTALQT	EQVQDSEHSG	KMVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAASDIKPD	KKRHAVISGS	VLYNQAEGKS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDQIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDQIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSKGMVAKRQFRIGDIAGEHTSFQDKLPEGGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSKGMVAKRQFRIGDIAGEHTSFQDKLPEGGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQQGHGKIEHLKSPENVDLAASDIKPDKKRHAVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQQGNKGIEHLKSPENVDLAADIKPDGKRHAVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	YSLGIFGGKAQEVAGSAEVTNNGIRHIGLAAKQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```

m742.seq
1  ATGTTTACG GCATTGCCGA AGCCGATGCG GCGGACAGCA GTGTGCTTAC
51  TTTGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTTTGTGCC CTGTGAAAT CAGAAACTG CCGGTTTCTG TTCAACGCTT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAAATACAA CCTTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAATATGC
351 GCGGGGTTTG TCGGGTGAGG ATGCGGTAGG CTTTTTGAAGT GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACCGCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGGCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCT AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTCGGGCGG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGAGG
1001 AGCCGGACCG CGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACACCGGTA
1201 TATGTCGATG TATATGAGCT GGACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACCGCTG CCTTTACCGG TTTTTCGGGT ACGGTGCCGG
1301 TTTGAAAAAC CGTCAAAGTG GCAGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGTA CTGCCAGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCACCT TTTGGGCGGG CTGCACTACA

```

```
1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTCGGCTA TGTTCCTGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTTCAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTC
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA
```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

m742.pep

```
1 MVYGIAEADA GDSSVLTLLG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
51 ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDPFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKDLDTG TYGLFGREHD FVVGAYAGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEPDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGRSTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNTNKT HSLTASTREN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

a742.seq

```
1 ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
51 TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCGTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GGCGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCCGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCCTA CGGCGATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA
```

```
1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGGAAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTGC GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGG ACAAACATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAG TCAACGCCGA
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 ACCCCGTGCA CATATTCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA
```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```
a742.pep
1  MVYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILSCEN QKTAPFSSTP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDECMSAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFGVYAYGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGEPDGDL S SPLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVMV ADDHVPALYN
451 YAKYLNTNKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQDNDVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEDWKVFAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFY G EPRTVSMKLD WQF*
```

a742/m742 98.5% identity in 783 aa overlap

```
10 20 30 40 50 60
a742.pep MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR
|||||
m742 MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR
10 20 30 40 50 60

70 80 90 100 110 120
a742.pep NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL
|||||
m742 NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL
70 80 90 100 110 120

130 140 150 160 170 180
a742.pep SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFNDNTAFEQYR
| |||||
m742 SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFNDNTAFEQYR
130 140 150 160 170 180

190 200 210 220 230 240
a742.pep SRRAAERKAGFDECMSAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP
```

1210

```
|||||:|||||:|||||:|||||:|||||:|||||:
m742      SRRAAERKAGFDKCMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQORFP
          190      200      210      220      230      240
          250      260      270      280      290      300
a742.pep  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          250      260      270      280      290      300
          310      320      330      340      350      360
a742.pep  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360
          370      380      390      400      410      420
a742.pep  RTVYAEECR NAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNP
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      RTVYAEECR NAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNP
          370      380      390      400      410      420
          430      440      450      460      470      480
a742.pep  GTPAFTGFSGTVPVWKT VKVADHDHPALYNYAKYLNTNKT HSLTAGTRFNV TGRHL LGG
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      GTPAFTGFSGTVPVWKT VKVADHDHPALYNYAKYLNTNKT HSLTAGTRFNV TGRHL LGG
          430      440      450      460      470      480
          490      500      510      520      530      540
a742.pep  LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
          490      500      510      520      530      540
          550      560      570      580      590      600
a742.pep  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
          550      560      570      580      590      600
          610      620      630      640      650      660
a742.pep  TVVDFGYVPGAGGKQGSFQTVAKPIGKVVS RGAEFELSGELNEDWKVFAGYTYNKSRYKN
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVVS RGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660
          670      680      690      700      710      720
a742.pep  AAEVNAERLAKNTGADPYNFSNFTP VHI FRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      AAEVNAERLAKNTGADPYNFSNFTP VHI FRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720
          730      740      750      760      770      780
a742.pep  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPR TVSMKLD
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPR TVSMKLD
          730      740      750      760      770      780
a742.pep  WQFX
          |||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNNTKTHSLTAGTRFNVVTGRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFNLTDLDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGFELEGRLNANIALYMKVRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGC GGTTCATGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCC
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC

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351  GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401  TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGCGCAA AATCGACGTG
451  TCTCCGAGTA CCGATTGGGC GGTATATGAC CATATTGAAG TTGTACGGGG
501  TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551  TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1  MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51  GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSLD DKAVHTLEEA
101  MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151  SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

	10	20	30	40	50	60
a743.pep	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT					
m743	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a743.pep	IDRMSTATGMRIAGKDTPQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
m743	IDRMSTATGMRIAGKDTPQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a743.pep	SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
m743	SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
	130	140	150	160	170	180
a743.pep	TVNLIRKR					
m743	TVNLIRKX					

g744.seq not found yet
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1  ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51  CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101  AATATTGGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
151  AAGGGAACTG GAAAGACAGC ATATGCTGTT TATTAACTA ATAACCTCTA
201  TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251  AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301  AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351  TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401  ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAAATTGTA
451  CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501  TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
551  CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601  GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATGTA
651  TGGGATAGAT ATTAGCCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701  GTGTAAAGG TCTTGCTAAC GCCATATGGA TGTTAAATAA TGATATCTTC
751  CCTTCCATTA AAGATAGTAA GGGGAAGGAT AGAGTTGTGT TATTGATTAG
801  ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAAACTTC
851  AAGATAATTC AGTATTTTAA GACTGGAGGA CGGATTATAA ATCTTATAGA
901  AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951  AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTAAAC TTCATTATT
1051 AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTG AAATTTTTTG AATTTTAAA CGGGAAAGAT AGATTTAAAT

```

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCCTTA AAGATAGAAA TTATGCAAAT
1501 ATTTCTCCTA AAATAAAAAC TGAAACTGAA TATTTAATAT TTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKLEFG FVDAANYRRR ENKDLFNRI VKGEYLDEL EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKEVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQO ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNQN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQOEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FOREYSIYLL
401 GEIKDHLLFY YSQSDYQNF KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLOFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFPFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTTA TCGTGCAGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTAAACGGC TGCATTGCAC
351 CAACCTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPIYRGTA DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPLV MKIREERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCGCCGCCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCTCAGTT CCGATCCTGC CGACAGCAAT
151 CCGCGACCGC AGGCCGGCGA AACGGGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCGGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACCGTA GCGCGCCGCG TGGTGCTGAT
351 TAACGACCGG CTGGAAGACA GCAACATCAA AGGTTTGGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTG GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

g746.pap

1	MSENKQNEVL	TGYEQLKRRN	RRRLVTASSL	VAASCILLAA	ALSSDPADSN
51	PAPQAQGETGA	TQSQTANTAQ	TPLKSAASLE	GETAADKKPD	LAGEDKPSAA
101	DEISEIPENV	GAPVLVINDR	LEDNSIKAGE	ESEKLQQAET	AKTEPKQAKQ
151	RAAEKVSATA	DSTDTVAVEK	PKRTAEPKPK	KAERTAEAKP	KAKETKTAEK
201	VADPKPTAAE	TKKPDTAESD	SAVKEAKKAD	KAEGKKTAEK	DRSDGKKHET
251	AQKTDRADKT	KTAEKEKSG	AGKKAAIQAG	YAEKERALSJ	QRKMKAAGID
301	STITEIMTDN	GKVVYRVKSS	YKNARDAERD	LNKLRVHGIA	GOVTNE*

m746.seq

1	ATGTCGCAAA	ACAACAAAA	CGAAGTCTGT	AGCGGTTACG	AACAACCTAA
51	ACCGGCGCAAC	GCGCGCGCCG	TGCTGACAGG	AAAGTTGCCTG	GTTGCCGCGCT
101	CTGTCATCTCT	GCTGGCAGCC	GGCTTCAGTT	CCGGCCCTGC	CGAACAGACT
151	GCCGGCGCAAA	CAAGCGGCGT	AGAAAAACAA	CGCGCAGGTG	CGGCACAAC
201	CAAGTCGCTT	AAATCCGCGC	CCGACAACCC	GCAGGACTTG	GCAGGCGAAG
251	ACCGCGCTTG	TGCCGCCGAC	AGCGAAATCA	CGCAGCTTGA	ACATCGTAGG
301	GCGCCGCTGG	TGCTGATTAA	CGAGCGCCTC	GAAGACAGCA	ACATCAAAAG
351	TTTGAAGACA	TCCGAGAAAC	TGCAACAGCG	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGCG	AAAAACAACG	GCTGCCGAAA	AAAGTCCGGC	AAGTCGCCAC
451	AGTAGCGGATA	CGGTAGCGGT	TGAAAAACCG	AAACGCACTG	CGGAAACAAA
501	ACCGCAAAAA	GCGGAAACGA	GTCGCCAAAG	CAAGCCCCAA	GCCAAAGAAA
551	CCAAAAACCG	CGAAAAAGTT	CGCGCAAAAC	CGAAACATGC	CGCCGAAAAA
601	ACCAAACCGG	ATACGGCAAA	ATCCGACAGC	GCGGTAAAG	AGCGCAAAAA
651	AGCCGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAAGAC	CGTTCCGACG
701	GCAAAAAACA	CGAAACGGCA	CAAAAAACCG	ACAAAGCGGA	CAAGACCAAA
751	ACCCGCGAGA	AGGAAAAATC	CGGTAAAAAA	CGCGCCATT	AGGCAGGTTA
801	TGCCGAAAAA	GAACGCGCCT	TAAGCCTCCA	GCGCAAAATG	AGGCGGCGG
851	GTATCGAATC	GACCATCAC	GAAATATATG	CCGACAACGG	CAAAGTTTAC
901	CGCGTCAAAT	CAAGCAACTA	TAAAAACGCA	AGGATGCGG	ACACGCGATT
951	GAACAAATTG	CGCGTACACG	GTATCGCGCG	TCAGGTAACG	AATGAATAG

m746.pcp

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILLAA	ALSSGPAEQT
51	AGETSGVENK	AAGAAQTPAL	KSAADKQPOL	AGEDKPSAD	SEISEPENVG
101	APLVLINERL	EDNSNLGLEA	SEKLQQAETA	KTAPKQAKQR	AAEKVPATAD
151	STDTVAVEKP	KRTAETKPKQ	AERTAKAKPK	AKETKTAEVK	ADKPKTAAEK
201	TKPDTAKSDS	AVKEAKKADK	AESKKTAEKD	RSDGKKHETA	QKTDKADKTK
251	TAEEKSGGKK	AAIQAGYAEK	ERALSRLQKM	KAAIGDSTIT	EIMTDNGKVY
301	RVKSSNYKNA	RDAERDLNKL	RVHGIAGQVT	NE*	

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

```

      10      20      30      40      50
m746.pep  MSENKQNEVLVSGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
g746      MSENKQNEVLVTGYEQLKRRNRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
      10      20      30      40      50      60
m746.pep  VENKAAGAAQTPALKSA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
g746      TESQTANTAQTPALKSAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
      70      80      90     100     110     120

```


1215

```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
      |||||
g746      LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ
      130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
      |||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
      190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRMKAAGID
      |||||
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRMKAAGID
      250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      |||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA  ACAACAAAA  CGAAGTCCTG  AGCGGTTACG  AACAACTCAA
51  ACGGCGCAAC  CGCGCGCGCC  TCGTAACGGC  AAGTTGCCTG  GTTGCCGCCT
101 CCTGCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151 GCGGCGGAAA  CAAGCGGCGT  AGAAAAACAA  GCGGCAGGTG  CGGCACAAAC
201 CCCTGCCCTT  AAATCCGCGG  CCGACAAACC  GCAGGACTTG  GCAGGCGAAG
251 ACAAGCCTTC  TGCCGCGGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301 GCGCCGCTGG  TGCTGATTAA  CGACCGCCTC  GAAGACAGCA  ACATCAAAGG
351 TTTGGAAGCA  TCCGAGAAAC  TGCAACAGGC  AGAAACCGCC  AAAACCGCAC
401 CGAAGCAGGC  AAAACAACGC  GCTGCCGAAA  AAGTGCCGGC  AACTGCCGAC
451 AGTACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACTG  CCGAAACAAA
501 ACCGCAAAAA  GCGGAACGCA  CTGCCAAAGC  CAAGCCCAAA  GCCAAAGAAA
551 CCAAAACCGC  CGAAAAAGTT  GCCGACAAAC  CGAAACTGCG  CGCCGAAAAA
601 ACCAAACCGG  ATACGGCAAA  ATCCGACAGC  GCGGTAAGAG  AAGCGAAAAA
651 AGCCGACAAG  GCTGAAAGCA  AAAAAACAGC  CGAAAAAGAG  CGTTCGGACG
701 GCAAAAAACA  CGAAACGGCA  CAAAAAACCG  ACAAAGCGGA  CAAGACCAAA
751 ACCGCCGAGA  AGGAAAAATC  CGGTAAGAAA  GCCGCCATTC  AGGCAGGTTA
801 TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGGCGG
851 GTATCGATTG  GACCATCACC  GAAATTATGA  CCGACAACGG  CAAAGTTTAC
901 CGCGTCAAAT  CAAGCAACTA  TAAAAACGCA  AGGGATGCCG  AACGCGATTT
951 GAACAAATTG  CGGTACACG  GTATCGCCGG  TCAGGTAACG  AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL  SGYEQLKRRN  RRRLVTASCL  VAASCILLAA  ALSSGPAEQT
51  AGETSGVENK  AAGAAQTPAL  KSAADKPQDL  AGEDKPSAAD  SEISEPENVG
101 APLVLINDRL  EDSNIKGLEA  SEKLQQAETA  KTAAPKQAKQ  AAEKVPATAD
151 STDTVAVEKP  KRTAETKPK  AERTAKAKPK  AKETKTAEKV  ADKPKTAAEK
201 TKPDTAKSDS  AVKEAKKADK  AESKKTAEKD  RSDGKKHETA  QKTDKADKTK
251 TAEKEKSGKK  AAIQAGYAEK  ERALS LQRM  KAAGIDSTIT  EIMTDNGKVV
301 RVKSSNYKNA  RDAERDLNKL  RVHGIAGQVT  NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      |||||
m746      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      10      20      30      40      50      60

```

1216

```

      70      80      90      100      110      120
a746.pep  AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
m746      AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
      70      80      90      100      110      120

      130      140      150      160      170      180
a746.pep  SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK
m746      SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK
      130      140      150      160      170      180

      190      200      210      220      230      240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
      190      200      210      220      230      240

      250      260      270      280      290      300
a746.pep  QKTDKADKTKTAEKEKSGKKAQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY
m746      QKTDKADKTKTAEKEKSGKKAQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY
      250      260      270      280      290      300

      310      320      330
a746.pep  RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
m746      RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      310      320      330

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```
          10      20      30      40      50      60
a747.pep  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR
          |||||
m747      LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR
          10      20      30      40      50      60
```

```
          70      80      90     100
a747.pep  HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
          |||
m747      HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
          70      80      90     100
```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272
Score = 59.3 bits (141), Expect = 6e-09
Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR 60
+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTLNKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
+T + E + GD + ++ EYG RV F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```
1 ATGAGTCAAA ACCAACC CGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCGCG
201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TCGGACGGCG ATTTGAGCCT GCAAATCTGC GCCTTACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAAACA CACCGCCCAA
601 ACCGCCGTC TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCCAAGGT TTCCGATCCC AAAACCGCGC ACGAGGTTTT ATGGACGGGC
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTCC CCAAAGACCC
951 CGAGGGTGAT ATCACGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACTGCC TCTTCCGCCG CGCCTACAGC
1051 TATTCTCGCG GACCCGCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAATC TTGCCGACGG TTTTATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251 GCTGCCGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```
1 MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKOGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPRQAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101 TQGGHEYQDGD DKLPSAGSGI LGKAFNPDGL TTVVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNDKLQKSW CDGDLQLQIC AFTPETCQTA LRDIKHTAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLOEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMLR ANPRDPEFLK KHCLFRFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG
```

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq
1 ATGAGCAAAA AACAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACGCTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTT CCGACGCTGA CCGCCCGCAT CGAGTTCTCT
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAAAC CACCGTCCAA
601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCGGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTAGGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG
751 GTGCCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
851 CGTTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAAATA CAGCGGTGCG
901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTTG CCAAGACCC
951 CGAGGGTGAT ATCAGGCCCA AAGACAGCCA TATACGCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACCGCC TCTTCCGCCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCG CGTGGA AAAA GCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep
1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQOAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGEYQDGD DKLPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLQLQIC AFTPETCQAA LRDIIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEOTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EYIISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

m748.pep	10	20	30	40	50	60
	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
g748	MSQNQPAQPT	KRNLFKTALA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
	10	20	30	40	50	60
m748.pep	70	80	90	100	110	120
	AGIVTPQOAF	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGEYQDGD	DKLPAGSGI
g748	AGIVTPROAF	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGEYQDGD	DKLPAGSGI
	70	80	90	100	110	120
m748.pep	130	140	150	160	170	180
	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK	KPIHLQEMRD	FSNDKLQKSW	CDGDLQLQIC
g748	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK	KTVHLQEMRD	FPNDKLQKSW	CDGDLQLQIC
	130	140	150	160	170	180
m748.pep	190	200	210	220	230	240
	AFTPETCQAA	LRDIIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP

a748.seq

1	ATGAGCAAAA	ACCAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAAA
51	CGCGATCGCA	GCTGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGGCGGCA
101	AAAAACGGGG	GGAACACGCC	GAACCGACCT	CCGAAGCCCA	ACACTCGGCC
151	CAAGCCTATC	CCTGCTACGG	CGAACATCAG	CGAGGCATCG	TTAGCGCGCA
201	GCAGGCGTTT	TCGATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCACGCTGA	CCGCGCCGAT	CGAGTTTCTC
301	ACCCAAGGCG	GCGAATACCA	AGACGGCGAC	GACAAACTTC	CGCAGGCGGG
351	CAGCGCGATT	TTGGGCAAA	CCTTCAACCC	CGACGGGTTG	ACCGTTACCG
401	TGGGGGTGGG	CAGCAGCCTG	TTTGACGGCC	GGTTGCGACT	CAAAAGCAAA
451	AAACCGATT	ATTTGAGGGA	AATGCGCGAC	TCTCCAAAG	ATAAGCTGCA
501	AAAAGCTGG	TGCGACGGCG	ATTTGAGCCT	GCAAATCTGT	GCCTTACACC
551	CCGAACCTGA	CCAAGCCGCC	TCGCGGCACA	TCATCAAACA	CACCGTCCAA
601	ACCGCGCTTA	TCCGCTGGAG	TATCGACGGG	TGGCAGCCTA	ATATCCGAAC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	TCTCCGCGAC	GGCAGGGCCA
701	ACCCCAAAGT	TTCCGAGCCCC	AAAACCTGCC	ACGAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	CAGACCTCGA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	TGAGTTTTGG	CAGACAGCGC
851	CGCTTCAAGA	GCAAAACCGA	ATTTTCGGGG	GGCGAAATA	CAGCGGCGCG
901	CCGATGGACG	CGAAAAAGA	AGCCGACCAA	CCGGATTTTT	CGGAAGACCC
951	CGAGGGGAAT	ACCAGGCCCA	AAGACAGCCA	TATAGCGCTG	CCCAATCCGC
1001	GCGATTCCGA	GTTCTCTAAA	AAACACCGCC	TCTTCCGCCG	CGCCTACAGC
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTGC	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAAAAC	TTGCGGACGG	ATTATCTCTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCGCTG	GAAGAATACA	TCAGCCCCCT	CGGCGGCGCG
1201	TATTTCTTCG	TCCTTGCCGG	CGTGGAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGG	GTATAA			

a748.pap

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGKKRGETA	ERTAESQHSP
51	QAYPCYGEHG	AGIVTPQAGF	LGKAFDVTDA	QSAQLENLF	RTLTARIEFL
101	TQGGEYQGDG	DLKPPAGSGI	SIMACPNVDL	TVTGVGSSL	FDGRFGLKDK
151	KPIHLQEMRD	FSNDKLQKSW	CDGDSLQIC	AFTPETCQAA	LRDI IKHTVY
201	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSPD	KTADEVLWTG
251	VAANSLDEFE	WAKNGSYQAV	RLRIHEVEFW	DRTLPEQQT D	IFGRRLXSGA
301	PMDGKKEADQ	PDFAKDPEGN	TTPKDSHIRL	ANPRDPEFLK	HKRLFRAYS
351	YSRGLASSGQ	LDVGLVFVCY	QANLADGFIF	VQNLNGEPL	EYISPFGGG
401	YFVFLPQVEK	GGFLGOGLLG	V*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSQPAYPCYGEHQ
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSQPAYPCYGEHQ
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGEYQDGGDKLPPAGSGI
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGEYQDGGDKLPPAGSGI
a748.pep	LGKAFNPDGLTVTVGVGSSLFDRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLQIC
m748	LGKAFNPDGLTVTVGVGSSLFDRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLQIC
a748.pep	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
m748	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
a748.pep	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA
m748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
m748	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
a748.pep	LDVGLVFVFCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLPGV EKG GFLGQGLLG
m748	LDVGLVFVFCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLPGV EKG GFLGQGLLG
a748.pep	VX
m748	VX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGCGGTT	CGGTCGGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGTTGT
201	GTTCATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGGCTTTCC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAG	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTCA	AGGCGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGCCACCCCG	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGTGTG	AAGACGACTT
651	CAAGACCGGT	GCGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC

1221

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801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAAC TG ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCGG TTGATTGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNL TALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPOPLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGA SEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCA GTAT CGCCGTC AAC
151 GACAATGCCT GCGAACCGAT GGAAC TGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGA CTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATT TGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAAC TTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAC TGATGA CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAC TG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCGG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNL TALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVS IAVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGA SEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep MRKFNL TALS VMLALGLTACQPPEAEKAAP AASGEAQ TANEGG SVS IAVN DNACEPMELT
          |||||
g749      MRKFNL TALS VMLALGLTACQPPEAEKAAP AASGETQ SANEGG SVGI AVN DNACEPMNLT
          10      20      30      40      50      60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVAD SGFKDTANEADLEKLPOPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAE LFS ELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATR VHYERIEPIAE LFS ELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVK EIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETA AKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSD FQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFQVNEILAKYRTK DGFETYDKLG					
g749	LSD FQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFQVNEILAKYRTK DGFETYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

```

1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCCGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAACCTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGA AAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 CACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

```

1  MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPLGS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEAD LEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD

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301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	MRKFNLTALSVMALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI	AVNDNACEPMELT
m749	MRKFNLTALSVMALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI	AVNDNACEPMELT
a749.pep	VPSGQVFNKNNSGRKLEWEILKGVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	
m749	VPSGQVFNKNNSGRKLEWEILKGVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD	
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD	
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK	DGFETYDKLG
m749	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK	DGFETYDKLG
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX	
m749	EADRKALQASINALAEDLAQLRGILGLKX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

1	GTGAAACCGC	GTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCGTG
51	TTCGCCCGAA	CCTGCCGCCG	AAAAAACTGT	ATccgCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgtcgcc	gtgtAcgaCt	ggGCGGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTTGCAG	CCTGCATTG	ACAAGGCGGC	AACGGTGGGG
301	ACGCTGTTTG	AGCCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCGCAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TTGAATGCGC	AGATTGACGC	GCTGTTTCGCC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCGG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCCGG	CTGCCGCCCG	TGGACGAATC	TTTACGCAAC	GAAGGGCAGC
701	GGCAGCCCGT	TTCTTCGAA	TACATCAAAG	AGAAAAACCC	CGGCTGGATT
751	TTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

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801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
851 AGCAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG
901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
951 AGAACCCGTT GCGGCGCAGT AG
```

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep

```
1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
51 VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLO PAFDKAATVG
101 TLFEPDCESL HRHNPQFVIT GPGAEAYEQ LAKNATTIDL TVDNGNIRTS
151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKKG RGLVLSVTGN
201 KVSAGTQSR LASWIHGDIG LPPVDESLRN EGHGQPVSE YIKEKNPGWI
251 FIIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
301 RQLIQAAEQL KAAFEKAEPV AAQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq

```
1 GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51 TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGCG GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA GCCGCCAAAG
551 GCAAAGGACG CGGGCTGGTG CTGTGCGTTA CGGGCAACAA GGTGTCCGCC
601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCTGTGA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC
751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTG AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
851 TCATGCCTGC CGCGAACTAC ATTGTGCGCG GCGGCGCGCG GCAGTTGATT
901 CAGGCGGCGG AGCAGTTGAA GGCGGCGTTT AAAAAGGCAG AACCCGTTGC
951 GGCGGGGAAA AAGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep

```
1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51 NPERVAVDW AALDTLTELG VNVGATTAPV RVDYLOPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSEFYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
301 QAAEQLKAAF KKAEPVAAGK K*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

```
10 20 30 40 50
m750.pep VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA-----ATLTVPTARGDAVVPKNPERVA
g750 VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVPTARGDAVVPKNPERVA
10 20 30 40 50 60
60 70 80 90 100 110
m750.pep VYDWAALDTLTELGVNVGATTAPVRVDYLOPAFDKAATVGTLFEPDYEALHRYNPQLVIT
g750 VYDWAALDTLTEPGNVGATTAPVRVDYLOPAFDKAATVGTLFEPDCESLHRHNPQFVIT
70 80 90 100 110 120
120 130 140 150 160 170
m750.pep GPGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA
```

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```

g750      GGPGAEEYELAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
          130      140      150      160      170      180

m750.pep  180      190      200      210      220      230
QTREAAKKGKRGVLVSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVVSFE
          190      200      210      220      230      240
g750      QKREAAKKGKRGVLVSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVVSFE
          190      200      210      220      230      240

m750.pep  240      250      260      270      280      290
YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNLDNALVRGTNAWKRKQIIVMPAANYIVAGGA
          240      250      260      270      280      290
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNLDNALVCGTNAWKRKQIIVMPAANYIVAGGA
          250      260      270      280      290      300

m750.pep  300      310      320
RQLIQAAEQLKAAFKKAEPVAAGKKX
          310      320
g750      RQLIQAAEQLKAAFKKAEPVAAQX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1   GTGAAACCGC  GTTTTTATTG  GGCAGCCTGC  GCCGTCCTGC  TGACCGCCTG
51  TTCGCCCGAA  CCTGCCGCGC  AAAAAACTGT  ATCCGCGCGA  TCCGCATCTG
101 CCGCCACACT  GACCGTGCCG  ACCGCGCGGG  GCGATGCCGT  TGTGCCGAAG
151 AATCCCGAAC  GCGTCGCGGT  GTACGACTGG  GCGGCGTTGG  ATACGCTGAC
201 CGAATTGGGT  GTGAATGTGG  GCGCAACCAC  CGCGCCGGTG  CGCGTGGATT
251 ATTTGCAGCC  TGCATTTGAC  AAGGCGGCAA  CGGTGGGGAC  GCTGTTTCGAG
301 CCCGATTACG  AAGCCCTGCA  CCGCTACAAT  CCTCAGCTTG  TCATTACCGG
351 CGGGCCGGGC  GCGGAAGCGT  ATGAACAGTT  GGCGAAAAAC  GCGACCACCA
401 TAGATCTGAC  GGTGGACAAC  GGCAATATCC  GCACCAGCGG  CGAAAAGCAG
451 ATGGAGACCT  TGGCGCGGAT  TTTCGGCAAG  GAAGCGCGCG  CGGCGGAATT
501 GAAGGCGCAG  ATTGACGCGC  TGTTGCGCCA  AACGCGCGAA  GCCGCCAAAG
551 GCAAAGGACG  CGGGCTGGTG  CTGTCGGTTA  CGGGCAACAA  GGTGTCCGCC
601 TTCGCCACGC  AGTCGCGGTT  GGCAAGTTGG  ATACACGGCG  ACATCGGCCT
651 ACCGCTGTGA  GACGAATCTT  TACGCAACGA  GGGGCACGGG  CAGCCTGTTT
701 CCTTCGAATA  CATCAAAGAG  AAAAACCCCG  ATTGGATTTT  CATCATCGAC
751 CGTACCGCCG  CCATCGGGCA  GGAAGGGCCG  GCGGCTGTCG  AAGTATTGGA
801 TAACGCGCTG  GTACGCGGCA  CGAACGCTTG  GAAGCGCAAG  CAAATCATCG
851 TCATGCCTGC  CGCGAACTAC  ATTGTCGCGG  GCGGCTCGCG  GCAGTTGATT
901 CAGGCGGCGG  AGCAGTTGAA  GGAGGCGTTT  GAAAAGGCAG  AACCCTTGCG
951 GCGGGGAAA  GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1   VKPRFYWAAC  AVLLTACSPE  PAAEKTVSAA  SASAATLTVP  TARGDAVVPK
51  NPERVAVYDW  AALDTLTELG  VNVGATTAPV  RVDYLQPAFD  KAATVGTLFE
101 PDYEALHRYN  PQLVITGGPG  AEAYEQLAKN  ATTIDLTVDN  GNIRTSGEKQ
151 METLARIFGK  EARAELKAQ  IDALFAQTRE  AAKGKGRGLV  LSVTGNKVSA
201 FGTQSRLASW  IHGDIGLPPV  DESLRNEGHG  QPVSFYEIKE  KNPDWIFIID
251 RTAAIGQEGP  AAVEVLNLDN  VRGTNAWKRK  QIIVMPAANY  IVAGGSRQLI
301 QAAEQLKEAF  EKAEPVAAGK  E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

```

a750.pep  10      20      30      40      50      60
VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVP TARGDAVVPKNPERVAVYDW
          10      20      30      40      50      60
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVP TARGDAVVPKNPERVAVYDW
          10      20      30      40      50      60

a750.pep  70      80      90      100     110     120
AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
          70      80      90      100     110     120
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
          70      80      90      100     110     120

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNI RTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNI RTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDESLRNEGHGQPV SF EYIKE					
m750	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDESLRNEGHGQPV SF EYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWK RKQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWK RKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAF EKAEPVAAGKEX					
m750	QAAEQLKAAFKKAEPVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

1	ATGGCTT	GTATGTT	GC	CACAACCC	AA	GCCGATAG	AG	CGGTAAGG	TC
51	TGCAACT	GC	CCTAAAG	AA	TGTGGTT	TCCA	TAAGAAG	ATA	ATAGATG
101	AAACAGG	TAA	AGTATCC	TT	GATACCAG	AC	AAATTTG	GTC	ATTGAAT
151	TTAAGCA	AGG	AAGAACT	GGC	AAGCATT	C	AA	GACACAA	ATG
201	TACTGTG	TCT	AATCCTG	GTA	TTTTC	AA	TAA	TCGAGA	AAGAT
251	ACGCAGC	AAA	ACAAAAT	CGT	AATAGT	AC	AA	ACGGTAG	TGG
301	GTATG	AA	CTCCAAC	AGG	GAAATAT	AAA	TCTGAT	TCTA	ATAACAA
351	AAAAGAT	TTT	TTATGGC	TCG	GTTCAAG	TCT	TGTTT	TCTG	AA
401	TCGGTTA	CGA	CCAATT	AAAT	AATAAAG	TGT	TCCAAG	GCTA	TTTACCC
451	ACCAATT	CAG	AAAACT	GAA	TCAAGAT	TAT	TATCGA	GAGG	TTCAAAA
501	GGGTAAC	GGC	TGGTCG	GTTG	ATACCAG	TAA	TCACAG	TCGT	GGGGGA
551	CAGCAAG	CGT	TTCTT	AAAA	GATTGGG	TAA	ACAATCA	AAAA	ACAAAAT
601	ATTGCC	CCCA	TCAGAAA	AGC	ACGTTT	CTAT	GGTAC	AGCC	CA
651	GAATGAT	TAC	GGCGAT	GTTT	TACAGAA	AAA	CGGCT	TATAC	C
701	CAGACGG	CAA	AACTTAT	AAC	AGCGGAT	CCT	ACTCA	ATCGT	GCATG
751	GATTTTG	TGG	GGAACAA	ATG	GATACCT	TTT	TTGCT	AGGAA	CCAATG
801	CACACA	AAGG	ACATGTA	AGG	GGTTGT	GCTA	TTGCA	TAGC	AGTTAT
851	CGGAGGT	GCC	AAAAGC	AGG	ACAAAAG	AAT	TTGATG	ACTA	TGTA </td
901	TGGGGT	GAA	TTGAAT	TGA	CGCTCA	AGG	AAGCCA	ATTA	ACAAAT
951	ACCCATA	CTG	GTAGA	ACCA	ACAAA	ACAA	AGATA	ATGAA	AAATAT
1001	AAGAAG	CTTT	CTAA						

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

1	MAWSMFAT	Q	ADRAVRS	A	PKEMWFH	KKI	IDDKT	GKVSF	DTRQI	WSLND
51	LSKEELAS	I	Q	DTNGKVI	TVS	NPGIFNN	RED	SLSNA	AQNR	NSTNGS
101	VMNPPTG	KYK	SDSNNKI	KDF	LWLGS	SLVSE	LMYVG	YDQLN	NKVFG	QYLPK
151	TNSEKLN	QDI	YREVK	MGNG	WSVDTS	NHSR	GGITAS	VSLK	DWVNN	QKQNG
201	IAPIRKA	RFY	GTATNV	QNDY	ADVLO	KNGYT	YTGAD	GKTYN	SGSYS	IVHDK
251	DFVGNK	WIPF	LLGTND	TTQG	TCKGL	CYSHS	SYFAE	VPKAG	TKEFD	DYVKI
301	WGEVEY	DAQG	KPINKS	KPIL	VEPNK	TKDNE	KYEKE	AF*		

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq..
  1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101  CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151  GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201  GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251  CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301  GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351  TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401  GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451  GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501  AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551  AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601  AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651  TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701  ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751  CGCGCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801  CAATAATACC TATGACGGCG TGGAAATCC GTTTATCCAT CCGTTGTCC
851  AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901  GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951  CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA ACAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
  1  MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
 51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101  EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151  EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201  KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251  PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301  GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351  DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401  RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451  SGNALFYVAP QDLLERLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
  1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101  CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151  GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201  GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251  CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301  GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351  TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401  GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451  GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501  AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551  AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601  AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
```

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```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTC TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCACTTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTC GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQALE GAATTRKVKAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGO FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIKRAVADL EHYISDKQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTGTC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIW WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCGCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAA ATTGACTGAA CGGGATTTGC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGCG ATGCAGACCA TCAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTGCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTTCG GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAA NEFLC MQTIKQAGIA VAQTSLS EDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQII RQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDV LDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKKTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATAGACCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```
1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQVRVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```
1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTTCGTG AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```
1 MTANFAQTLV EIQDSLVRV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFMQIGRRSY
151 SREDISEANR RAERVPYGA E LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```
1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTTCGTG AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```
1 MTANFAQTLV EIQDSLVRV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFMQIGRRSY
151 SREDISEANR RAERVPYGA E LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLVRVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLVRVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAAC TGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADE	LQYVWEHTAVTDHQGKLVEI	PVCYGGGEYGPDLAEVAAFHQ			
a758	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADE	LQYVWEHTAVTDHQGKLVEI	PVCYGGGEYGPDLAEVAAFHQ			
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMM	GFQPGFPYLGGLPEALHTPR	RAVPRTSVPAGSVGIGGSQT			
a758	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMM	GFQPGFPYLGGLPEALHTPR	RAVPRTSVPAGSVGIGGSQT			
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELP	LFRADLNPPTLLAAGDQVRF	VAERIEPX			
a758	130	140	150	160		
	GVYPFASPGGWQIIGRTELP	LFRADLNPPTLLAAGDQVRF	VAERIEPX			

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTTCCTGCT CTTACTCATC CATTGTCCGC AACGATGTGC
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTACCGGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCACAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACC GCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGA AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
 651 AAACCACGGC TTA CTGCTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTGACAAAG
 751 CATGAAAACC GCTGGGTGCT TGGGGCGTA CTCAGCACCT ACGCCGGCTT
 801 CGATAATTTT TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
 901 GAACTCATAT GGC GCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
 951 CAACGAACGC ATCACCCTGC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCACT TCGACAGCAA CTTACCGTTC GTCCGTAATA
 1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCCAAA AAGCTGCTTC AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
 1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTTC TACCATATC
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCT
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA
 1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC
 1701 CGGCGGCAAC CCGCGCGAAT TTTTCCCCTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTGGG
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
 1901 AAGCAGCCAT AGAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCAGCTGTG TGCTCAACGG CGGCATGAAC CTTAACGGGG
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTAGGCGAG GCCCGTACCC
 2101 CATGCCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG
 2351 TTTTAAAAGC CGAAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
 2551 GACGGCGCAC AAATTACCCG GAACCCGAT TTCGCCAATA ATACACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCGGCA
 2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAACCTGGAAG GGGACAGCCG CGGCGCATTC CAAATCCACG TCAAAAACAC
 2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCATTGTG AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTCAACC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAAA AACAAACAACG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
 3151 CGTGCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGTGTAAGAA TGGCCGAATC CGAATTGAC
 3301 AAAGCACGGC AAGGCGGCGA TCGCAAGCC GTCGAAACAG CCCGGCACGC
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAATC GATCAGCCGG
 3451 TCGGCCAACA CCGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAAC TACCAACTAT GCACATATCG GCATCCAAAC
 3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1   MRFTHTTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51  GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLL G NGQPKANAYL DTD RFPYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGT P LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER I TLP IANPSL APQND SRHMP SEDAGKTLIL
351 SSRFDNK TLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKL GAGTL IANGQGINQG DISIGETVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRLDL NGNNLAFTHI
501 RHADGGAQIV NHNPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLLNGGMN LNGEV LIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQKGTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLGKAHLYGS IRAGKDTAVR MEADSNWTL S QSSHTGALT L
851 DGAQITLNP D FANNT HNNRF NTLTVNGTLD GFGTFRFLT G IVRKQNA PPL
901 KLEGDSRGAF QIHVKNTGQE PQTTE SLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVOYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAELISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE D GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAANGT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KOAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1   AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51  CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCG GGTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCGCG GTCCGGCGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1   NNRNTRYAAL GKRVMEGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51  DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1   ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGCGACG CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTC GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCG GACCAAAAGC TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GGCGCGTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GGCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAAATGC ACAGCCACGA CGTGTTCCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCTTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTTCCGCG CTTTGCCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCCG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCTCT TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCGA TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTTCGTTC TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAAACCGT TACGCGCAT TGGGCAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAAATCCA TGCAGTTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGACGGGAT ACATGCAGGC
1951 GGTTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATT CCGGTTGCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1   MGQFMSVERI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQOVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFAFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGLYQQRRL LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNTYFA GSKLNNTGQA DVAGLGTDIK
351 QKAFAVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLSKSVAlD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYFYRMKDKNAAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAI	TPKW	
				10	20	30

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPCLKLQINADNIFNRHYARVGSESTFNIPGSESLTANL					
	:			:		
g760	AGMHAGGYATFDAMAAYRFTPCLKLQINADNIFNRHYARVGSTNTFNIPGSESLTANL					
	100	110	120	130	140	150

	709
m760.pep	RYSFX
g760	RYSFX

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

```

m761.seq
1  ATGAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51  CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGCC
301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTCCT TCGCGGTTT
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC
451 CCGTCTTCCG TGCTTTACGG CCGCACC AAC GCGCGCGCG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT
551 ACGGCTCATG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAAATC
651 GTTCCGCAGC GGCATAGACA GCAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGG
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCGATTG AAATTCTGTC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGCGCG
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTTCAACGC CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGCGTGGA

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1701  ATTGTCCGCC  ATCGGGCAAA  TCATCCCCAA  AAAACTCTAT  CTGCGCGGTT
1751  CGTTGGGCGT  GATGCAGGCG  AAAGTCGTTG  AAGACAAAGA  AAATCCCGAC
1801  CGAGTGGGCA  TCCATTTGAA  TAATACCAGC  AACGTTACCG  GCAACCTGTT
1851  TTTCCGTTAT  ACCCCGACCG  AAAACCTCTA  CGGCGAAATC  GGCCTAACCG
1901  GTACAGGCAA  ACGCTACGGT  TACAACCTAA  GAAATAAAGA  AGTGACTACG
1951  CTTCCAGGCT  TTGCCCCAGT  TGATGCCATG  CTTGGCTGGA  ACCATAAAAA
2001  TGTTAACGTT  ACCTTTGCCG  CAGCCAATCT  GCTCAATCAA  AAATATTGGC
2051  GTTCGGACTC  TATGCCGGGT  AATCCGCGCG  GCTATACTGC  CCGGGTAAAT
2101  TACCGTTTCT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
1  MKISFHLALL  PTLIIASFPV  AAADTDNNGE  HYTATLPTVS  VVGQSDTSVL
51  KGYINYDEAA  VTRNGQLIKE  TPQIDTLNI  QKNKNYGTND  LSSILEGNAG
101  IDAAYDMRGE  SIFLRGFQAD  ASDIYRDGVR  ESGQVRRSTA  NIERVEILKG
151  PSSVLYGRTN  GGGVINMVS  K  YANFKQSRNI  GAVYGSWANR  SLNMDINEVL
201  NKNVAIRLTG  EVGRANSFRS  GIDSKNVMVS  PSITVKLDNG  LKWTGQYTYD
251  NVERTPDRSP  TKSVDYDFGL  PYRMGFAHRN  DFKVDKLQVW  RSDLEYAFND
301  KWRAQWQLAH  RTAAQDFDHF  YAGSENGNLI  KRNYAWQOTD  NKTLSNLT
351  NGDYITGRFE  NHLTVGMDYS  REHRNPTLGF  SSAFSASINP  YDRASWPASG
401  RLQPILTQNR  HKADSYGIFV  QNIFSATPDL  KFVLGGRYDK  YTFNSNKLT
451  GSSRQYSGHS  FSPNIGAVWN  INPVHTLYAS  YNKGFPYGG  RGGYLSIDTL
501  SSAVFNADPE  YTRQYETGVK  SSWLDDRLST  TLSAYQIERF  NIRYRPDPKN
551  NPYIYAVSGK  HRSRGVELSA  IGQIIPKKLY  LRSLGVMQA  KVVEDKENPD
601  RVGIHLNNTS  NVTGNLFFRY  TPTENLYGEI  GVTGTGKRYG  YNSRNKEVTT
651  LPGFARVDAM  LGWNHKNVNV  TFAANLLNQ  KYWRSDSMPG  NPRGYTARVN
701  YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
1  ATGAAAATAT  CATTTCATTT  AGCTTTATTA  CCCACGCTGA  TTATTGCTTC
51  CTTCCCTGTT  GCTGCCGCCG  ATACGCAGGA  CAATGGTGAA  CATTACACCG
101  CCACTCTGCC  CACCGTTTCC  GTGGTCGGAC  AGTCCGACAC  CAGCGTACTC
151  AAAGGCTACA  TCAACTACGA  CGAAGCCGCC  GTTACCCGCA  ACGGACAGCT
201  CATCAAAGAA  ACGCCGCAAA  CCATCGATAC  GCTCAATATC  CAGAAAAACA
251  AAAATTACGG  CACGAACGAT  TTGAGTTCCA  TCCTCGAAGG  CAATGCCGGC
301  ATCGACGCCG  CCTACGATAT  GCGCGGCGAA  AGCATTTTCC  TGC GCGGCTT
351  TCAAGCCGAC  GCATCTGATA  TTTACCGCGA  CGGCGTACGC  GAAAGCGGGC
401  AGGTGCGCCG  TAGCACCGCC  AACATCGAGC  GCGTGGAAAT  CCTGAAAGGT
451  CCGTCCTCCG  TGCTTTATGG  GCGTACCAAC  GCGCGCGGTG  TCATCAACAT
501  GGTCAGCAA  TACGCCAACT  TCAAACAAAG  CCGTAATATC  GGTACGGTTT
551  ATGGTTTCGTG  GGCAAACCGC  AGCCTGAATA  TGGACATCAA  CGAAGTGCTG
601  AACAAAAACG  TCGCCATCCG  TCTACCGGC  GAAGTCGGGC  GCGCCAATTC
651  GTTCCGCAGC  GGCATAGACA  GCAAAAATGT  CATGGTTTCG  CCCAGCATT
701  CCGTCAAAC  CGACAACGGC  TTGAAGTGGA  CGGGGCAATA  CACCTACGAC
751  AATGTGGAGC  GCACGCCGCA  CCGCAGTCCG  ACCAAGTCCG  TGTACGACCG
801  CTTCCGACTG  CCTTACCGCA  TGGGGTTCGC  CCACCGGAAC  GATTTTGTCA
851  AAGACAAGCT  GCAAGTTTGG  CGTCCGACC  TTGAATACGC  CTTCAACGAC
901  AAATGGCGTG  CCCAATGGCA  GCTCGCCAC  CGCACGGCGG  CGCAGGATTT
951  TGATCATTTC  TATGCAGGCA  GCGAAAATGG  CAACTTAATC  AAACGTAAC
1001  ACGCCTGGCA  GCAGACCGAC  AACAAAACCC  TGTCGTCCAA  CTTAACGCTC
1051  AACGGCGACT  ACACCATCGG  CCGTTTGTAA  AACCACCTGA  CCGTAGGCAT
1101  GGATTACAGC  CGCGAACACC  GCAACCCGAC  ATTGGGTTTC  AGCAGCGCCT
1151  TTTCCGCCTC  CATCAACCCC  TACGACCGCG  CAAGCTGGCC  GGCTTCGGGC
1201  AGATTGCAGC  CTATTCTGAC  CCAAAACCGC  CACAAAGCCG  ACTCCTACGG
1251  CATCTTTGTG  CAAAACATCT  TCTCCGCCAC  GCCGATTG  AAATTCTGTC
1301  TCGGCGGCCG  TTACGACAAA  TACACCTTTA  ATTCCGAAAA  CAAACTCACC
1351  GGCAGCAGCC  GCCAATACAG  CGGACACTCG  TTCAGCCCCA  ACATCGGCGC
1401  AGTGTGGAAC  ATCAATCCCG  TCCACACACT  TTACGCCTCG  TATAACAAAG
1451  GCTTCGCGCC  TTATGGCGGA  CGCGGCGGCT  ATTTGAGCAT  CGATACGTTG
1501  TCTTCGCGCC  TGTTCAACGC  CGACCCCGAG  TACACCCGCC  AATACGAAAC
1551  CGGCGTGAAA  AGCAGTTGGC  TGGACGACCG  CCTCAGCACT  ACGTTGTCTG
1601  CCTACCAAAT  CGAACGCTTC  AATATCCGCT  ACCGCCCCGA  TCCAAAAAAC
1651  AACCCTTATA  TTTATGCGGT  TAGCGGCAAA  CACCGTTCGC  GCGGCGTGGA
1701  ATTGTCCGCC  ATCGGGCAAA  TCATCCCCAA  AAAACTCTAT  CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCGGACCG AAAACCTCTA CGGCGAAATC GCGCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGA CTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLENQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

```

m761.pep      10      20      30      40      50      60
MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA
|||||
a761          10      20      30      40      50      60
MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA

m761.pep      70      80      90      100     110     120
VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD
|||||
a761          70      80      90      100     110     120
VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD

m761.pep     130     140     150     160     170     180
ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNNGGGVINMVSKYANFKQSRNI
|||||
a761         130     140     150     160     170     180
ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNNGGGVINMVSKYANFKQSRNI

m761.pep     190     200     210     220     230     240
GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG
|:|||||
a761         190     200     210     220     230     240
GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG

m761.pep     250     260     270     280     290     300
LKWTGQYTYDNVERTPDRSPTKSVYDRFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND
|||||
a761         250     260     270     280     290     300
LKWTGQYTYDNVERTPDRSPTKSVYDRFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND

m761.pep     310     320     330     340     350     360
KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDKTLSSNLTNGDYTIGRFE
|||||
a761         310     320     330     340     350     360
KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDKTLSSNLTNGDYTIGRFE

m761.pep     370     380     390     400     410     420

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m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLQPILTQNRHKADSYGIFV
a761       NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLQPILTQNRHKADSYGIFV
           370      380      390      400      410      420

           430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
           430      440      450      460      470      480

           490      500      510      520      530      540
m761.pep  YNKGFPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
a761      YNKGFPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
           490      500      510      520      530      540

           550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761      NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
           550      560      570      580      590      600

           610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
           610      620      630      640      650      660

           670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761      LGWNHKNVNVTFAAANLNFNQKYWRSDSMPGNPRGYTARVNYRFX
           670      680      690      700

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g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGCG
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLFIFNEV TKSIIYMAIY PILYFFTICK YYPYSRKVII LLSLALSIFY
101 SFMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGCG
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIIYMAIIY PIIYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTAC CTGCGGCTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GCGCGAGCAA CATTGCGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
 251 CAGTGC GCGC ACGGCAACAA CAAGCCAAGG CCGCATTCC TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTGCG CGCTTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGT
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCAGCTGG AAGTAATACG GGCGCGGCGAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACGG TATTTGCGGA
 1401 ATAA

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```
1 MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51 SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQROP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVG YQN NLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```
1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACG GTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCG CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCCGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGC GCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCGG TATTTCGCGA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```
1 MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51 SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQROP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVG YQN NLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

m763 / a763 99.8% identity in 467 aa overlap

```
10 20 30 40 50 60
m763.pep MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
|||||
a763 MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
10 20 30 40 50 60
```

1242

	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSAADFQASHYQORDAVRARQQQAKAAFLPHVSVANASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSAADFQASHYQORDAVRARQQQAKAAFLPHVSVANASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAIDTANLLARYLPKLERYSLEDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLEDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNLYTSSAQNNDYHYRGKGMSVGVQLNLPLYTGGELSGKIHEAEA					
a763	QNSRYPTVSAHVGYNLYTSSAQNNDYHYRGKGMSVGVQLNLPLYTGGELSGKIHEAEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

m764.seq

```

1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAAGT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGTTTTTGG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGCGG
251 CTTCGGGCAA AACGGTGTCG GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CCGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACCGGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

m764.pep

```

1   MFFSALKSFL SRYITVWRNV WAVRDQKPP KRTAEEOAFL PAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSA LRGHQ AELQSAKAE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAADD DKMDVEVLVL NKDIGFEVQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

a764.seq (partial)

```

1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAAGT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGTTTTTGG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGCGG
251 CTTCGGGCAA AACGGTGTCG GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA

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1244

```

701 CAGCAGACTA CCGCCGTTTG CGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTGAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGGTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

a764.pep (partial)

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVVDGQHVKGGE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVVDGQHVKGGE					
	70	80	90	100	110	120
m764.pep	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
	130	140	150	160	170	180
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQKLVSVAIEQQKTADYRRL					
a764	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQKLVSVAIEQQKTADYRRL					
	190	200	210	220	230	240
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
	310	320	330	340	350	360
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT					

1245

```
|||||
a764 DKMDVEVLVLNKGDFVEQGDVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
      370      380      390      400      410      420

      430      440      450      460      470
m764.ppep AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFREXR
          |||||
a764 AVVSLDKHTLNIDGK
          430
```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```
m765.seq
1 ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51 GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGCGCGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCCG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGCG CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```
m765.pep
1 MLRCRPKSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
51 ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGKKNVQOQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGYGLTL PYSRSLIEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLIPTVM PVYEQSVRNK
301 GRVNRKRRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```
a765.seq
1 ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51 GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGACGGG TCGTTGCTGA TGTTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCCG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```
a765.pep
1 MLRCRPKSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
```

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```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLT DGEIAAI MGHEMTHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLPTVM PVYEHSVRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPSVLDSDGIFLKFNF	FLRSKPKYEISFLPSFKRIL	CLSAVISVLGACAVVADVYG			
a765	MLRCRPSVLDSDGIFLKFNF	FLRSKPKYEISFLPSFKRIL	CLSAVISVLGACTVVADVYG			
	10	20	30	40	50	60
m765.pep	HDSATMNAAA	AKDYMKTVELNKSAGNVDTT	SRTARRVQAVFRRMLPYADA	ANNTSHKFDW		
a765	QDSATMNAAA	AEDYMKTVELNKSAGNVDTT	SKTARRVQAVFRRMLPYADA	ANNTGHKFDW		
	70	80	90	100	110	120
m765.pep	KMTVFKNDEL	NAWAMPGGKMAFYTGIVDKL	KLTDDEIAAIMGHEMTHALH	EHGKKNVQOK		
a765	KMTVFKNDEL	NAWAMPGGKMAFYTGIVDKL	KLTDGEIAAIMGHEMTHALH	EHGKKNVQOK		
	130	140	150	160	170	180
m765.pep	ILTNMAAQIG	TQIILDKKPD	TNP	ELVGLGMDILGTYGLTLP	PYSRSL EEEA	DEGGMMLMAQ
a765	ILTNMAAQIG	TQIILDKKPD	TNP	ELVGLGMDILGMYGITLP	PYSRSL EEEA	DEGGMMLMAQ
	190	200	210	220	230	240
m765.pep	AGYHPAAAVR	VWEKMNQENDQNGFIYAIT	STHPTNNARIE	NLKRLPTVM	PVYEQSVRNK	
a765	AGYHPAAAVR	VWEKMNQENDQNGFIYAIT	STHPTNNARIE	NLKRLPTVM	PVYEHSVRNK	
	250	260	270	280	290	300
m765.pep	GRVNKNRRR					
a765	GRVNKNRRR					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTTG TTGGATAAAC
101 CCATTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGG TACATTGCCA TCATTTTCGAT CCTTTGTAT TGAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGGAACAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCCGCG TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAGAATT GGTGCAAAA
601 GTCAGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQP GKIEVLEFFG
51  YFCVHCHHFD PLLKLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKA VYEQKIR LENRAVAGKW ALSQKGF DKG KLMRAYDSPE
 151 AAAVALKMQK LTEQY GIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCCTCA AGAACAGTCG GGTA AAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGCTGGC
 251 AGCCTGAAAT GCTCGGTTT GCTAGGATGG CGGCTGCCGT CAATTGTGCG
 301 GGT TTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAAAACA GGTCGGTTGC CGAAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
 451 GCTGCCGCCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTGCGCAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQS GKIEVLEFFG
 51 YFCVHCHFD PLLKLGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
 101 GLKYQANPAV FKA VYEQKIR LENRSVAGKW ALSQKGF DKG KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	SAVLSAQAYAL	TEGEDYLVLD	KPIPOEQSPG	KIEVLEFFGY	FCVHCHFD
m767	MKFKHLLPLL	SAVLSAQAYAL	TEGEDYLVLD	KPIPOEQSGK	IEVLEFFGY	FCVHCHFD
	10	20	30	40	50	60
	70	80	90	100	110	120
g767.pep	PLLLKLGKAL	PSDYLRTHEV	VWRPEMLGL	ARMMAAVKLS	GLKYQANSV	FKAVYEQKIR
m767	PLLLKLGKAL	PSDAYLRTEH	VVWQPEMLG	LARMAAVNLS	GLKYQANPAV	FKAVYEQKIR
	70	80	90	100	110	120
	130	140	150	160	170	180
g767.pep	LENRAVAGKW	ALSQKGF DKG	KLMRAYDSPE	AAAVALKMQK	LTEQY GIDST	PTVIVGGKYR
m767	LENRSVAGKW	ALSQKGF DKG	KLMRAYDSPE	AAAAALKMQK	LTEQYRIDST	PTVIVGGKYR
	130	140	150	160	170	180
	190	200	210			
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCCTCA AAAACAGTCG GGCA AAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAATGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGCTGGC
 251 AGCCTGAAAT GCTCGGTTT GCAAGAATGG CTGCTGCGGT CAAGCTGTCA
 301 GGT TTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAAAACA GGTCGGTTGC CGAAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTACGA CTCTCTGCG

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOKQS GKIEVLEFFG
51  YFCVHCHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFQDG KLMRAYDSPA
151 AAAAAASKMQQ LTEQYRIDST PTVVVGKRYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767 96.7% identity in 214 aa overlap

a767.pep      10      20      30      40      50      60
MKLKHLLPLL SAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD
|||||
m767          10      20      30      40      50      60
MKLKHLLPLL SAVLSAQAYALTEGEDYLVLDKPIPOEQSGKIEVLEFFGYFCVHCHHFD

a767.pep      70      80      90      100     110     120
PLLLKLKALP SDAYLRTEHV VVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR
|||||
m767          70      80      90      100     110     120
PLLLKLKALP SDAYLRTEHV VVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR

a767.pep      130     140     150     160     170     180
LENRSVAEKW ALSQKGFQDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKRYR
|||||
m767          130     140     150     160     170     180
LENRSVAGKW ALSQKGFQDGKLMRAYDSPAAAAALKMQKLTEQYRIDSTPTVIVGGKRYR

a767.pep      190     200     210
VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
|||||
m767          190     200     210
VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKOLITAA LIASAAFATQ AAPQKPVSA QTAQSAVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCGCGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPOKPVSAQAQHSADVWIDVRSEQEFSEGHHLHNAVNIP					
	:					
m768	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHPAVWIDVRSEQEFSEGHHLHNAVNIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIEAAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX					
	:					
m768	VDQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGC AAAAACCCGT ATCCGCGGCC CAAACCGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
 201 CATAACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSADVWI DVRSEQEFSE
 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHSADVWIDVRSEQEFSEGHHLHNAVNIP					
	:					
m768	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHPAVWIDVRSEQEFSEGHHLHNAVNIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX					
	:					
m768	VDQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTATTTTT TGTGGGAAGA CATTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAgaAAC ACCgtgCGAA CCGGATTGTA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCTG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCCATT ACCGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGTTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAACA GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACG CGGGCGGCGA
801 CGTGTCGGCG AGGTTTTATC CGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCGACA ATACCCATT GCAAATTTCC AATTCGCTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTTAC CCGGAGCGCA
1151 ACCCCGCGCA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCAAG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAG AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC TGTCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQGVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPQL MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQOY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNWV YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNWQOT PRWQTLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WGQEWGSGSL SSLFRLGVAK RHYEKPFFS SFKGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 GCGGGAAGAA GGAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGGAAATTGAT TGCCGCCCAA
451 CCCGACGCGC CCGCGTCCG TATGCGTTTG CCGGCAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACCGC ATGCGTGGA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CCGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGGCAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAAACCCG AAATGGCAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC

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1251

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1251  GGC GAAACGG CATTATGAAA AACCCGGCTT TTCAGCGGT TTTAAAGGGG
1301  AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACC GG
1351  GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACC GCGA
1401  AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451  TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
1    LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51   HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSVVSN
101  IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151  PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201  RERDAWKVNG GFSVTREHNI NQAPKRQOYG KWTFPKQVDG TAVNYRLGAE
251  KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301  AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351  SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401  GQEWGSGSL SLLRLGAAKR HYEKPGFFSG FKGERRRDK E LNTSLSLWHR
451  ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769    95.1% identity in 492 aa overlap

          10      20      30      40      50      59
g769.pep    LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAEETPCEPDLSRPEFRLHEAEVKPI
          |||||  |||||  |||||  |||||  |||||  |||||
m769        LIMVIFY--FCGKTFMPARNRWMLLLPLLASAAYAEETPREPDLSRPEFRLHEAEVKPI
          10      20      30      40      50

          60      70      80      90     100     110     119
g769.pep    DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
          60      70      80      90     100     110

          120     130     140     150     160     170     179
g769.pep    KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD
          120     130     140     150     160     170

          180     190     200     210     220     230     239
g769.pep    RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQQYGNWTFPKQV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQQYGNWTFPKQV
          180     190     200     210     220     230

          240     250     260     270     280     290     299
g769.pep    DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        DGTAVNYRLGAEEKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
          240     250     260     270     280     290

          300     310     320     330     340     350     359
g769.pep    GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI
          300     310     320     330     340     350

          360     370     380     390     400     410     419
g769.pep    SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLFRLGVA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLRLGAA
          360     370     380     390     400     410

          420     430     440     450     460     470     479
g769.pep    KRHYEKPGFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
          |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep   KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAGTTT TGCAGATTGA CGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCCGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGGAATTGAT TGTCGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAATT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACCGC ATGCGTGGAA GGTAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAGCCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGCGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTCG ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 GCTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GGGGAAACGG CATTATGAAA AACC CGGCTT TTTACGCGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGTGAT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTG TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKROQYG KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAAR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

```

1253

```

|||||
m769      EKVPGQVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
              70          80          90          100         110         120

              130          140          150          160          170          180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAVAVRMRLAAALFENRQNEAAADQFDRL
              130          140          150          160          170          180

              190          200          210          220          230          240
a769.pep   KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFFPKQVDG
|||||
m769      KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFFPKQVDG
              190          200          210          220          230          240

              250          260          270          280          290          300
a769.pep   TAVNYRLGAEEKWLSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKWLSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250          260          270          280          290          300

              310          320          330          340          350          360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGLKNTRRARSNDNTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGLKNTRRARSNDNTHLQISN
              310          320          330          340          350          360

              370          380          390          400          410          420
a769.pep   SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLLRLGAAKR
|||||
m769      SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLLRLGAAKR
              370          380          390          400          410          420

              430          440          450          460          470          480
a769.pep   HYEKPGFFSGFKGERRRDKELNLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
|||||
m769      HYEKPGFFSGFKGERRRDKELNLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
              430          440          450          460          470          480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AAGCGCGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAAT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTC CAACCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1   MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKRGTFGA FKSRIQVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

```

1254

```

101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACCAGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

m770.pep

```

1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSRIQVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

```

              10      20      30      40      50      60
g770.pep      MNRLLLLSAAVLP TACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA
              |||||
m770           MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA
              10      20      30      40      50      60

              70      80      90      100     110     120
g770.pep      KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPK EVFKRGTFGFAFKSRQIVRY
              |||||
m770           KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPK EVFKHGASFAFKSRQIVRY
              70      80      90      100     110     120

              130     140     150     160     170     180
g770.pep      DPKRKAFAVLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDG VQADTSGKLLAGACIISNPI
              |||||
m770           DPKRKTFAVLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDG VQADTSGNLLAGACMISNPI
              130     140     150     160     170     180

g770.pep      KNPDKRX
              :| |||
m770           ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

a770.seq

```

1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACCAGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

a770.pep

```

1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSRIQVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

```


151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKFVKHGASFAFKSRQIVRY
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKFVKHGASFAFKSRQIVRY
a770.pep	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDG VQADTSGNLLAGACMISNPI
m770	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDG VQADTSGNLLAGACMISNPI
a770.pep	ENPDKRX
m770	ENLDKRX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTGAAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTGCTCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCACGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTGCCC
1201	GCAAAATTCA	AATATACGCG	GGAAGGCGCA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAACCC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	CGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGCCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCGG

```
1751 GGAAAATCTC GGGCAGCACA CCCTTCTACC GATTACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA
```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```
g771.pep
1 MDLLSVFHKY RLKYAVAVLT MLLLAUVGLH ASVYRTFTPE NIRSRLQQSI
51 AHTHRKISFD ADIRRRLLFR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRRI
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQOFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNGLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQPVA
401 AKFKYTREGA PHLEAAAAAQ KLNLA PYLDE FRQNGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTASGENRK
551 QLIRSLQGS LSNISNGAWH GIDMSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```
m771.seq
1 ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGTGTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAGCATT
151 GCACACACAC ACCGGAAAAT CTCGTTTGAT GCGGCATTTC AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TTGAAAAAAC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 TCGAAAAACA GCACGTCCTG CCTCAATTTC CTGACGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGT TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTC GAAGCTTCCA CTTCTGCTGA CCGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 GCCCAAAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCCCGGCTC GTATGGACGG AAAACAAAGG GCTGGACGGC
1051 CCGCGCCTGT ATGTATCGAC CTTTCAAGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTC AGGGCTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGGCA CGCGGTATC GACCTGACCG CGGGCGGCGA AACC CGAAAA
1651 GAGCTTATCC GTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCCG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCTTCCA CCGATTACG
1801 CTCAACAGCG AAATTTTACA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTCTCCGAC AGCCTCTATG TTACCGACAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGC ACGGTGGACA AACC GTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRHKISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRHKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVS					
m771	ADIQRLLPRPTVILKNLTITEPGGDQAVSVQETKIGLSWKNLWSDQIQIEKWVVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQQLILKEISLNLSQ					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNLSQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQQFESSGILVWRKLSVPWKSRGLFLSDGIGTPEISPFHFEASTSLDGHGITIST					
m771	GQPFESSGILVWGKLSVPWKSRGLFLSNGIGPPEISPFHFEASTSLDGHGITIST					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGFTTAGGEY					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNSIKIETVNGAFTTAGGEY					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDNGLDAPRLH					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLY					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTDFDRQPVAAKFYRTREGAPHL					
m771	TVNRLPQPRFISRLDGSLSVPNLQNWNAELNGTDFDRQTVAAKFRYTHEDAPHLE					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KLNLAPYLDEFRQQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLH					
m771	KLNLTPYLDDVRQQNGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLH					

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNLSGKISG---STPFYRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHDITELFSDSLVYTSNGYTNLDTQELSEDVLRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHDITELFSDSLVYTSNGYTNLDTQELSEDVLRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

1	ATGGATTAT	TATCGGTCTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTAGC
51	CGTGTGACG	ATACTGCTTT	TGGCGGCAAT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCATCTT	CACACCTGAA	AACATCCGAA	GCCGCTCCCA	ACAAAGCATT
151	GCCCATACGC	ACCGGAAAAT	CTCGTTGAT	GCGGATATAC	AGCGCAGGCT
201	TCTGCCCCGG	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	GCGGCGACCG	GACTGCCGTT	TCCGTCCAAG	AAACCAAAAT	CGGATTGAGC
301	TGGA AAAACC	TGTGGTCGGA	TCAGATACAG	ATTGAAAAAT	GGGTGGTTTC
351	GAGTGCGGAA	CTTGCCCTGA	CGCGCGACGG	GAAAGGTGTT	TGGAACATCC
401	AAGACCTGAT	CGACAGCCAA	AAACGCCAAG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGGAAC	AGCTTATCCT
501	GAGGAAATC	AACCTCAACC	TGCAATCCCC	CGATTCTGTC	GGGCAGCCGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGGGAA	AGCTGTCCGT	CCCGTGAAAA
601	AGCAGGGGGC	TGTTCTCTTC	AGACGGCATC	GGCAGCCCCA	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATTACCATTT
701	CCACCAACCG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGCGCG	AGCGGATGCC
751	GCCGCGCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCCCAAAAT	CCTACGCTGG	CACTCAGGAA	CAACAGCATT	AAAATTGAAA
851	CCGTC AACCG	CGCATTACCC	GCCGCGCGCG	AATATGCCCA	ATGGGACCGT
901	TCGTTC AAAC	TCGACAAAGC	CAACCTGCAC	TCCGCGATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCAC	CAGACCAACT
1001	TCTCCCTCAA	TTCCGCGCTC	GTATGGACGG	AAAACAAAGG	GCTGGACCGG
1051	CCGCCCTGTG	ATGTATCGAC	CCTTCAGGAT	ACCGTCAACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCGTA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	AACCGTTGCC
1201	GCGAAATTCA	GATACACACA	TGAAGACGCA	CCGCATCTGG	AAGCCGCCGT
1251	CGCACTGCAA	AAATTGAACC	TGACCCCTA	TCTTGACGAC	GTGCGGCAAC
1301	AAAACGGCAA	AATATTTCCT	GACACCCTCG	CCAAGCTGTC	CGGCGACATC
1351	GAGGCGCAC	TGAAAATCGG	AAAAGTCCAA	CTTCCCGGCC	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGGCCATATC	CGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	CGCGGTCATC	GACCTGACCG	CGGGCGGCGA	AACCCGAAAA
1651	GAGCTTATCC	GCTCGCTTCA	GGGCAGCCTG	TCGCTAAATA	TTTCCAACGG
1701	TGCATGGCAC	GGTATCGACA	TGGACAATAT	CCTGAAAAAC	GGCATTTCGG
1751	GCAAACTGTC	CGACAATGCC	GCACCCAGCA	CACCCCTCCA	CCGATTACAG
1801	CTCAACAGCG	AAATTTCAGA	CGGCATCAGC	CGCCACATCG	ATACCGAACT
1851	CTTCTCCGAC	AGCCTCTATG	TTACCGCAA	CGGCTATACC	AATCTGGATA
1901	CGCAGGAATT	GTCTGAAGAT	GTCCTTATCC	GCAACGCCGT	CCATCCGAAA
1951	AACAACCCGA	TTCCCTGAA	AATACCGGT	ACGGTGGACA	AACCGTCCAT
2001	TACCGTCGAT	TACGGCAGGC	TGACCGGCGG	CATCAATTCC	CGCAAGAGAG
2051	AACAGAAAAT	CCTCGAAGAC	ACCCTGCTGG	AACAATGGCA	GTGGCTCAAA
2101	CCTAAGAAGC	CGTAA			

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

a771.pep

```

1  MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
51  AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQWNNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTGGGSI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDQTQELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
701 PKPE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLLLAAGLHASVYRIFTPE	NIRSRLQOSIAH	THRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPE	NIRSRLQOSIAH	THRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE		
m771	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE		
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS		
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS		
a771.pep	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHF	EASTSLDGHGITISTTGSPS	
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHF	EASTSLDGHGITISTTGSPS	
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG		
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG		
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD		
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD		
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQWNNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ	
m771	TVNRLPQPRFISRLDGSLSV PNLQWNNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ	
a771.pep	KNLNTPYLDDVRQONGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGHI	
m771	KNLNTPYLDDVRQONGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGHI	

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNLIKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNLIKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```
g772.seq
1      GTGTTTCGGCA  CGGTCTTGCG  GACTGATGCC  GACTGCCTGC  AAATCATCGT
51     CGTCGGGCAAT  TTCTTTTCAG  TTGTTTCGTA  TGGTTTTTGC  GCGTTTGGCG
101    AAGGCGAGTT   TCACCAAGTT  GGCAGAAATG  TCGAAATCGT  GCGCCTTGCC
151    GATACGGTGT   TTCACGGGAA  TCATGCGCAC  CACTGCGGAA  TCGATTTTCG
201    CGCGCGGGAT   GAACGATTTC  GGGCGGCACG  CAATCAGCAG  CTCATATATC
251    AAAAAAATATT  CGACATATCA  ACCCAAGCGA  CCGTAGTCGT  TGCTTTTTCG
301    CGCGGCAACC   ATGCGCTCGA  CCACTTCTTT  TTGCAACATA  AAGTGCATAT
351    CGGCGACATC   GTCGCGCCAC  TCCGCCAGTT  TGAACAAAAG  CGGCGTGGAG
401    ATGTTATACG   GCAGGTTTCC  GCGATTTTTC  TTTTTGCGTG  AGATGCGCGT
451    GAAATCAAAC   TGCAACATCG  GAGCTTCGTG  AATCACCAGT  TTATCCGCAA
501    ACGGCAGCGT   TTTCAGACGG  CATACGATGT  CGCGGTCGAT  TTTCGACAAC
551    TGCAGGCGGT   TCACTTTTTT  CGCCAAAGGT  TCGGTAATTG  CCGCCAAACC
601    CGGGCCGATT   TCAATACAGA  CATCATCCGC  CTGCGGGGCG  CCGCGATTGA
651    CAATATCCGC   GATAATCCGC  GTGTCTGTCA  AAAAATCTGT  CGCGCAATCG
701    TTGCGGGCCT   TGTGTTCTTT  CATCGTGTTT  CCTCTTCGGT  TGAAACCCCG
751    CCTTTTAGGG   CGGCAGGATA  AGACTCTGTT  TGGGCGGGGC  GCTAACCCCT
801    CCAATACAGG   ACGACACATA  GGGCGTGCTT  TTATGTGTGC  TTCTGTGTGT
851    TGGAACATAA   ATGTGTTTAC  AGTATCCGTT  TGATGTCGGC  ATTGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pap

1	VFGTVLRTDA	DCLQIIVVGK	FFQVYVAYGFA	ALAEGEFHQF	GMTEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	EFRGRHVNQQ	LHIEKILQHH	QTATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGVDVIRQA	DDFLFA*DAV
151	EIKLQHVAVF	NHQFIRKQR	FQTAYDVAVD	FDNVQAVOLF	RQRFGNCRQT
201	RADFNHDIIR	LRAHGVDNIA	DNPRVLQKIL	PETLAGVFVF	HRVSSSVETP
251	PFRAGSDSV	WAGRNPFQIR	THRAVLVYS	SCVLEHKCVY	SIRLMSLA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```
m772.seq
1 ATGTTCCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGTTTTCGCG CGCTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GGCAAAATGC TCGAAATCGT CGCCTTTCGC
151 GATGCGGGTG TTAACCGGAA TCATACGGAG GACGGCGGAA TCCACTTTCG
201 CGCAGAGGTT GAACGATTCT GCGGGTACGT CAATCAGACT TTCCATATCG
251 AAAAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTTCG
301 CGCGGGCAAC ATACGCTCGA CCACCTCTTT TTGCAGATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAG CGGTGTGAA
401 ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTGCCTG CGATGCCGTT
451 GAAATCAAC TGCAATACAT CGCCTTCGTG AATCACAGT TTATCCGCA
501 ACGCGACCGT TTTACAGCGG ATACAGATGT CGCGGTGCAT TTCGACAACG
551 TCGAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGGCCGAT TCAATCACGA CATCATCCGC GTGCGGGCGC CCGGCTGTGA
651 CAATATCGCT GATAATCCGC GTGCTCTGCA AAAAATTTCT CGCCGAACG
```

m772.pgp

1	MFGAVLRID	DCLQIIVACK	LFQIVAYGFA	ALVEGEFHEF	GKMLEIVRLA
51	DAVFNHRNTH	DGGIHFRRRV	ERFRGVNQH	FHIEKILQH	AQAADVVAFR
101	RGNHTHDHF	LQKHVHIDDI	VHRLRVLEQ	RCGNVVREVA	DDFLFACDVA
151	EIKLQYIAFV	NHQFIRKRQR	FQTAVDVAVD	FDNVQAVOLF	RQRFGNRRQT
201	RADFNHDIIR	LRAHGVDNIA	DNPRVLQKIL	PETLAGVFFF	HRVSFSVETP
251	PFRAVESDSI	WEGRNSFQIR	MAHRAVLVYS	CVLKHKCVY	SLRMSAL*

Homology with a predicted ORF from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

1	ATGTTCGGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTFCAG	TTGTTGCGTA	TGGTTTTGCG	GGGTTGGTGG
101	AAGCGGAGTT	TCACGAGTTT	GCAGAAATGC	TCGAAATCGT	CCGCGTTGCC
151	GATACGGGTG	TTTACCGGAA	TGATCGGGAC	GACGGCCGAA	TCGACTTTCC
201	GCGCGGGGTC	GAACGATTCC	GGCGGCACGT	CAATCAGCAT	TTCCATATCG
251	AAGAAATATT	CGAGATCATC	CGCCAAACGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGCAACTC	ATACGATCGA	CCACTTCTTT	TTGCAGCAT	AAGTGCATAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAG	CGCGGTGAA
401	ATGTTGTAGG	GCAGGTTGCC	GACGATTTTC	TTTTTGCGTG	CGATGCCGTT
451	GAATCAAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTGCACAACG
551	TGCAGGCGGT	TCAGCTTTTG	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGACCGGAT	TCAATCACTA	CATCATCCGC	CTCGCGGCCG	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCTCTGA	AAAAAATTCT	CCGGAACCGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTT	CCTTTTCGGT	TGAAACCCCG
751	CCCTTTAGGG	CGGTAGAATC	AGACTCTAAT	TGGGAGGGGC	GTAACCTCCT
801	CCAAATCAGG	ACGGCACATA	GGGCGGTGCT	TTATGTGTCG	TCTGTGTGTG
851	TGAAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTGAA

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
  1 MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
 51 DTVFHRNHAD DGRIFHRRGV ERFGRHVNQH FHIEEILQHH AQAAVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLOYIAFV NHQFIRKQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKL	FQIVAYGFAALVEGEFHEFG	EMLEIVRLADTVFHRNHAD			
m772	MFGAVLRIDADCLQIIVACKL	FQIVAYGFAALVEGEFHEFG	KMLEIVRLADAVFHRNHAD			
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRIFHRRGV	ERFGRHVNQH	FHIEEILQHH	AQAAVVVAFR	RGNHTIDHFF	LQHKVHIDDI
m772	DGGIHFRRR	VERFGRYV	NQHFI	EIKLQHH	AQAAVVVAFR	RGNHTLDHFF
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQK	RRGNVVGQVADDF	LFACDAVEIK	LQYIAFVN	NHQFIRKQR	FQTAYDVAVD
m772	VRHLRQLEQK	RCGNVVRE	VADDFLFACDAVEIK	LQYIAFVN	NHQFIRKQR	FQTAYDVAVD
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLF	RQRFGNRRQ	RTDFNHDIIR	LRAHGVNDI	ADNPRVLQKIL	PETLAGFVFF
m772	FDNVQAVQLF	RQRFGNRRQ	TRADFNHDIIR	LRAHGVNDI	ADNPRVLQKIL	PETLAGFVFF
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETP	PPFRAVESDSI	WEGRNSFQIR	TAHRVLYVS	SCVLKHKCVY	SIRLMSALX
m772	HRVSFSVETP	PPFRAVESDSI	WEGRNSFQIR	MAHRVLYVS	SCVLKHKCVY	SIRLMSALX
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
  1 ATGGGATTGG GTGCAACGAC TTTGTGCGGT TCGGGTGCTA TAGGCGGAGG
 51 TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATTT TAAACATTT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGCGAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```


This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLTPK TADVQRNLS QSEVGKWK GIEGQMPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGYIDK
201 TANFKSYELS EVPLRADMIK OREIHLAIPA QTNKEQRLQL QRVVEYGKSO
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAATGTGTA AACGGGAAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
651 GATACAGACC TATCCCGGCA GCCCGCGCGC AAAACGCGCC GCCGCAGCCG
701 TACGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCGCGCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTGCA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGCAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRLDYLEGKI				
m774	MKIKLPLFIIWLSVSASCASVSPVAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGKI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGRTYVQK	LDDRKLKEHYLNTEGGSSAHTVETAQN				
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQK	LDDRKLKEHYLNTEGGSSAHTVETAQN				
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGDGG	SIAQRSMYLLQSRARMGNCSVIEIGGRY				
m774	LYNQALKHYKSGKFSAAASLLKGADGGDGG	SIAQRSMYLLQSRARMGNCSVIEIGGRY				
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQOKDIAR	TWRSLIQTYPGSPAAKRAAAVRKRX				
m774	ANRFKDSPTAPEAMFKIGECQYRLQOKDIAR	TWRSLIQTYPGSPAAKRAAAVRKRX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACCGC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCACTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCTTCCAG	CAGGGCATAC	GTCCAAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTGTC	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAACC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGCGCGAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFII	WLSVSAACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLDDRKLK
101	EHYLNTEGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAAS	LLKGADGGDG
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT	APEAMFKIGE
201	CQYRLQOKDI	ARATWRS LIQ	TYPGSPA AKR	AAAAVRKR*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRNIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT					
m774	MKIKLPLFIIWLSVSASCAS-VSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK					
	10	20	30	40	50	

1265

```

          70      80      90      100      110      120
a774.pep  LVRLSNEVELNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m774      IVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
          60      70      80      90      100      110

          130      140      150      160      170      180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGG SIAQRSMYLLQLSRARMGNCE SVIEIGGR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m774      NLYNQALKHYKSGRFSAAASLLKGADGGDGG SIAQRSMYLLQLSRARMGNCE SVIEIGGR
          120      130      140      150      160      170

          190      200      210      220      230      239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTPGSPA AKRAAAAVRKRX
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m774      YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTPGSPA AKRAAAAVRKRX
          180      190      200      210      220      230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGGCCCTT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACTCACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGTTGCTG GAGTCAAAAA ACGGTTTATG TCCGCGGCAC AGGCAAGAAG
851 CGGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGACGCCG GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AA AEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSR
51  YSNMFIGSSW KSPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTHNH SDADGKALSM
151 RLTPRFLSLD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPHP RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPV NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGGCCCTT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACTCACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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1266

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACCGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTTCGATTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCR
51 YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDITI NNHHTHTHNH SDADGKALSM
151 RLTPRPLLSR RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPHP RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

a790.pep	10	20	30	40	50	60
	MARRSKTFEEAAEEVEERFGHRGIKLVFEFEGTAKPCVINC PKHGNQTCRYSNMFIGSSW					
m790	MARRSKTFEEAAEEVEERFGHRGIKLVFEFEGTAKPCVINC PKHGNQTCRYSNMFIGSSW					
	10	20	30	40	50	60
a790.pep	70	80	90	100	110	120
	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII					
m790	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV					
	70	80	90	100	110	120
a790.pep	130	140	150	160	170	180
	LNDVQGDITI NNHHTHTHNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
m790	LNDVQGDITI NNHHTHTHNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
	130	140	150	160	170	180
a790.pep	190	200	210	220	230	240
	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID					
m790	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPAEDI ALIELSDKRLVVAHLVID					
	190	200	210	220	230	240
a790.pep	250	260	270	280	290	300
	IAGRMLIYQT GRPSEALD LPEGSVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI					
m790	IAGRMLIYQT GRPSEAFD LPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI					
	250	260	270	280	290	300
a790.pep	310	320	330	340		
	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC					
m790	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGT TT
51  TGGTTTGT TT TTTGGTTTTT GTGTATTTGG AGTGGGTC TG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGCT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTTAT TCGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGAAT TACAAAAATC GGCGATTTC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGT GCGCGGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTAG CGCGCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTG
1151 ACAGGCGCGC CTGCGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAATG
1201 GGGGAGGACC GTATCCGCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGBA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTGCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCGGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTGCG CGCCCAATG CAACCTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGTCAGG TGTGGTCCGT GTCGGTACGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG GCGCGCAACC TTCCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

g791.pep

```

1 MVNYYSAMIK KILTTCTFGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQ
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTTRKF
151 NEVLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLNG LPKAPSAYNP IVNPERAKLR QKYILNMML EKMIVTQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDMKMPA VVLDTVKKKK VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPILLQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI VGGYAQOYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQ QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVT A VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKGK MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

m791.seq

```

1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAATGCCGTT GACTATTTAT TCGGCGGATG
151 TACGACCTTA AAATGCCGTT GACTATTTAT TCGGCGGATG GCGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GCGGATTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCGGCGGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGCGGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTC
601 ACTTTGGCGG AAGCCGCCAT GCTTGGCGGA CTGCCCAAGG CTCCGCTGTC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCGGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGTCGG CGGTTATGAT
1351 TTTACAGCA AAACATTCAT TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGGCTCATC AGTGTTTAA GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CCGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTGCGTT ACGCGCAAC ATATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGC CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG CAGGTTGCG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAACCGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 CCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA AGCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTAA

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLOH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDEV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF ARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQ ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPKGK
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAF QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKGG MKMPEGVVS NGEYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

g791/m791 97.3% identity in 805 aa overlap

	10	20	30	40	50	60
g791.pep	MVNYYSAMIKKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY					
m791	MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY					
	10	20	30	40	50	60
g791.pep	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS					
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS					
	70	80	90	100	110	120

1269

g791.pep	130	140	150	160	170	180
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
g791.pep	190	200	210	220	230	240
	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPLKAPSAYNPVNPRAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPLKAPSAYNPVNPRAKLRQKYILNNMLE					
	190	200	210	220	230	240
g791.pep	250	260	270	280	290	300
	EKMITVQQORDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFKVYTTV					
m791	EKMITVQQORDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV					
	250	260	270	280	290	300
g791.pep	310	320	330	340	350	360
	RTDHQKAATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVP					
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVP					
	310	320	330	340	350	360
g791.pep	370	380	390	400	410	420
	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGAVIRVKNNNGRW					
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNNGRW					
	370	380	390	400	410	420
g791.pep	430	440	450	460	470	480
	AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLQALGSLDAKTGAVRALVGGYDFHSTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
g791.pep	490	500	510	520	530	540
	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
g791.pep	550	560	570	580	590	600
	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
g791.pep	610	620	630	640	650	660
	DRDGRRLRAQMPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
g791.pep	670	680	690	700	710	720
	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRVGGYGGTIAVPVWVDYMRFALKGKGKQKG					
m791	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRVGGYGGTIAVPVWVDYMRFALKGKGKQKG					
	670	680	690	700	710	720
g791.pep	730	740	750	760	770	780
	MKMPEGVVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
g791.pep	790	800				
	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAATGCCCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCCGT GACTATTTAT TCGGCGGATG GGGAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGT GCGCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTTG AGCAGTGAAA AACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTC
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC GCATTACGAG CGGTTTGTTC GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT GCGCGCAGCA GCTACCGCGG TGCGGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTCCCGGCC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CCGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG CTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGTTTAA GCATGCCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG CAGGTTGCG CGCCAAATG CAACCTTTTG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GCGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGACAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTT GCGCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CCGGGCGGAA GCGGACGCG AGGCGGCGGA TGACGAAGT CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDLSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKREY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEXYGEDAY TQGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKV VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 FHSRIRRGAV IRVKNNGGRW AVVQEPLLGQ ALVSLDARTG AVRALVGGYD
451 FEDSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPKGG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSSLP ASLSMALGTG ETTPLVKVEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAKGTG TNDNKDAWF VGFPDVTVA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKGG MKMPEGVVSS NGEYYMKERM VTDPLTLN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPV LPSNTGSKQQQ
801 LDSLF*
```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNERAKLRQKYILNNMLE
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
	RADHQKVATEALRKALRNFRGSSYRGAENYIDLKSEDEVEETVSQYLSGLYTVDKMVPA
m791	RADHQKVATEALRKALRNFRGSSYRGAENYIDLKSEDEVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
	VVLDTVTKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
m791	VVLDTVTKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
	AVVQEPLQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
m791	AVVQEPLQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
	GVGYAQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
m791	GVGYAQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
	DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGKTG
m791	DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
	TTNDNKDAWFGFNPDDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG
m791	TTNDNKDAWFGFNPDDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
	MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGAAEGGRQAADDEV
m791	MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGAAEGGRQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLP	SNTGSKQQQL	DSLFX			
m791	RQDMQETPVLP	SNTGSKQQQL	DSLFX			
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CGggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACC CGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GTTGCCTCAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGG GGCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCTCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cggcaaatTA ccccaaacgg aaacggactg
701 attgttccag atattgaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAA KLTVLVPAPF
201 YYSDBPKSKR LRNKTNIIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GGCATTACC GCGATGATGG AAGCCGTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATTT AAACCTCAATC GAATGGCACT ACGGCgTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAACA GCAGGCGGCA AAACCTGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1  MFRIIKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHPKSKR LRNKTNIIVLK RMGSALPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK					

[illegible]

```
a792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGCTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGTGAAGCA GTTTGAACAG
151 GAAGTGCGCG ATGTCGCACT GGATTACCGC TGGATTGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGCGACGG CGGCTTCGAT TGGGGCGGCA TTCAAACAGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGTGCAGCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAAG
401 CGGAAGAAGC GGGCATTAAC CGGATGATGG AAGCCGTTAC CGACAAGAAG
451 AGGATTTTTG AACTGTATTT AAATCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA CGCGGCTCCC GGTATTTTTA TCAAAATACC CGCCGCAAGC
551 TGACCAAACA GCAGGCGGCA AAGATGACGG CGCGCTGCC CGCCGCGTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGCAT
701 GA
```

a792.pap

1	MFRIIKWLIA	LPVGIFIFFEN	AVVYGNIIITY	RAVAPHGRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRISTN	LKKALIAED	ARFAGHGDF	WGGIQNAIR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNSI	EWHYGVFGAE	AASRYFYQIP	AAKLTQKQAA	KLTRVPAFL
201	YYADHPKSKR	LRKNKTINVL	RMGSALFES	DTD*	

a792.pep	10	20	30	40	50	60
	MFR	I	K	W	L	I
m792	MFR	I	K	W	L	I
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
	W	M	P	Y	K	R
m792	W	M	P	Y	K	R
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
	N	L	F	L	N	S
m792	N	L	F	L	N	S
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
	A	A	K	L	T	A
m792	A	A	K	L	T	A
	190	200	210	220	230	

g793.seq

1274

```
1 ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51 GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTGTTTGGCC TGTCTGATTG CCGCGGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC GTGCCGAGCT
351 TGTCGATGTG CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTC CGGGACCGGC AGGGCAATAT
651 TTGGGACAGC TTGGACTCCC CGCGCAATAA AGCACCAGCA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGCG CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCTCTTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGCGCGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAACCCGGC
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCAGGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCCGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```
1 MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51 TVTYNFLKEQ GDNRIVRTQA LPATRGTVSD RNgAVLALSA PTESLFAVPK
101 DKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM KXSNVGTSK LSAREFGAEM YDFYHELIG VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYTALT HDGVLLPLSF
451 ERQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVVGAKTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYYGGVVA
551 GPPFFKIMGG SLNILGISPT KPLTAAAVKT PS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```
1 ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51 GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTGTTTGGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC GTGCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGCG CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
```

1275

```
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCAGACCG GCGGCGACCG
1451 GTACGGCGGG TCGGTTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```
1 MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51 TVTYNFKLKEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKIG PPSVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRWR RPIEQATMSF GYGLQLSLLO LARAYTALTH DGVLLPVSE
451 QAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAVKTP S*
```

g793/m793 98.5% identity in 582 aa overlap

g793.pep	10	20	30	40	50	60
m793	10	20	30	40	50	60
g793.pep	70	80	90	100	110	120
m793	70	80	90	100	110	120
g793.pep	130	140	150	160	170	180
m793	130	140	150	160	170	180
g793.pep	190	200	210	220	230	240
m793	190	200	210	220	230	240
g793.pep	250	260	270	280	290	300
m793	250	260	270	280	290	300
g793.pep	310	320	330	340	350	360
m793	310	320	330	340	350	
g793.pep	370	380	390	400	410	420
m793	360	370	380	390	400	410

1276

```
          430      440      450      460      470      480
g793.pep   FGYGLQLSLLQLARAYTALTHDGVLLPLSFKEQAVAPQGKRIFKESTAREVRNLMVSVTE
           |||||||||||||||||||||:||||||||||||||||||||||||||||||
m793       FGYGLQLSLLQLARAYTALTHDGVLLPVSFEQAVAPQGKRIFKESTAREVRNLMVSVTE
           420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep   PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
           |||||||||||||||||||||:||||||||||||||||||||||||||||||
m793       PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
           480      490      500      510      520      530

          550      560      570      580
g793.pep   AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX
           |||||||||||||||||||||:||||||||||||||||||||||||||||||
m793       AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX
           540      550      560      570      580
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```
a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCTTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTTGT TTTGAAAAAG AATTAAAAACG
501 CCATTACCCG ATGGCAACCC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CCGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TCGGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCCTTC GGTACGGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGCGCG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGCGGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTT
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```
a793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  LVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPAAQ LERLSELVDV PVDVLRNKLE QKGKSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFHVGIG FTDIDGKQOE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRNRN
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALH DGVLLPVSFE
451 KQAVAPQGR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFKKIMGGS NLILGISPTK PLTAAVKTP S*
```

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793						
	10	20	30	40	50	60
	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793						
	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
a793.pep	130	140	150	160	170	180
	PVDVLRNKLKLEQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793						
	130	140	150	160	170	180
	PVDVLRNKLKLEQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793						
	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
a793.pep	250	260	270	280	290	300
	ORIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
m793						
	250	260	270	280	290	300
	ORIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793						
	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793						
	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQGKRIKKESTAREVRNLMVSVTEP					
m793						
	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQGKRIKKESTAREVRNLMVSVTEP					
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793						
	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLGISPTKPLTAAAVKTPSX					
m793						
	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLGISPTKPLTAAAVKTPSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTCCCCTACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTAT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGCA
451 CCCGTTTCA ATCAGGAAAA CTGCTTGCC GTCCACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTCCGCCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGCGGAC GGCAAACGTC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CCGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCGCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGCGCGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRMLMD HSLWGEVGSF DHFEADSGSP
201 FMTFPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENSGLSLRKE
401 RVTARMMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAC AAGCCGGCCC GCGGCCACAG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCTCGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTCA ATCAGGAAAA CTTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCCGCC
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGCGGAC GGCAAACGTC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CCGGCCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCGCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCCG GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGCGCGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV

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1279

101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
 151 PVFNQENLLD AQKQLREQGI LNITGHLMLD HSLWGEVGSF DDFEADSGSP
 201 FMTFPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
 251 AACPSIKKLM RASFSDNTLK LRGNIPECL GKPVGVMFA LDELIRQSFT
 301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSNLI
 351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLV ENGSGLSRKE
 401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
 451 TGTNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
 501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

g794.pep	10	20	30	40	50	60
	VRFNHFMVTIIIVISPAKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLLL					
m794	10	20	30	40	50	60
	VRLNHFMIAIIIVISPAKPARRHVSPTYPALPYNCFYVTDLPMNFPKTAASLLLLL					
g794.pep	70	80	90	100	110	120
	ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS					
m794	70	80	90	100	110	120
	ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
g794.pep	130	140	150	160	170	180
	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRLMLD					
m794	130	140	150	160	170	180
	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGILNITGHLMLD					
g794.pep	190	200	210	220	230	240
	HSLWGEVGSFDFEADSGSPFMTFPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	190	200	210	220	230	240
	HSLWGEVGSFDFEADSGSPFMTFPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
g794.pep	250	260	270	280	290	300
	QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVMFALDELIRQSFT					
m794	250	260	270	280	290	300
	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVMFALDELIRQSFT					
g794.pep	310	320	330	340	350	360
	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTD MNKRSNLIARSVFLKLGGD					
m794	310	320	330	340	350	360
	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTD MNKRSNLIARSVFLKLGGD					
g794.pep	370	380	390	400	410	420
	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMETAYFSPFA					
m794	370	380	390	400	410	420
	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMETAYFSPFA					
g794.pep	430	440	450	460	470	480
	QDFIDTLPIAGTDGTLRNRFKQSGGLRLKGTGLNNVRALAGYWLGDKPM AVVVIINSGR					
m794	430	440	450	460	470	480
	QDFIDTLPIAGTDGTLRNRFKQSGGLRLKGTGLNNVRALAGYWLGDKPM AVVVIINSGR					
g794.pep	490	500	510			
	AVSLLPDLNDFVAKNIISGGDWLDKLMCKERRAX					
m794	490	500	510			
	AVSLLPDLNDFVANNIISGGDWLDKLMCKERRAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
 51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
 101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
 151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
 201 GCTCGATACA GGTGCGATTG CGCAAACGA AATCGCCGTA TATGTCCAAG
 251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGCTC

1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGCGAG AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCCGCC
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTTCCGA GAGCTGTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTCGCG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGCGCGCG AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCGCTCT TCCTCAAAC CCGCGCGGAC GGCAACTGC CCGCCGTTTC
1101 CGAACAGGCA CCGTCTGCCG TCCGGCGTGA ACTTGCCTG TCGGCATCG
1151 ATGTGCGGA TTTGGTTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCGGTTTCCC
1451 TGTGCCCCG CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGGCG
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRLREQGI RNITGHLMLD HSLWGEVGS DDPEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

a794.pep	10	20	30	40	50	60
m794	10	20	30	40	50	60
a794.pep	70	80	90	100	110	120
m794	70	80	90	100	110	120
a794.pep	130	140	150	160	170	180
m794	130	140	150	160	170	180
a794.pep	190	200	210	220	230	240
m794	190	200	210	220	230	240
a794.pep	250	260	270	280	290	300
m794	250	260	270	280	290	300
a794.pep	310	320	330	340	350	360
m794	310	320	330	340	350	360

m794	NHWLLGGGRISDGIIGIADTPEGAQTLAVAHAKPMKEILTD MNKRS DNLIARSVFLKLGDD	310	320	330	340	350	360
a794.pep	GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMM AQMLETAYFSPFA	370	380	390	400	410	420
m794	GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMM AQMLETAYFSPFA	370	380	390	400	410	420
a794.pep	QDFIDTLPIAGTDGTLRNRFKQSGGLRLRLKTGT LNNVRALAGYWLGD KPM AVVVI INSGR	430	440	450	460	470	480
m794	QDFIDTLPIAGTDGTLRNRFKQSGGLRLRLKTGT LNNVRALAGYWLGD KPM AVVVI INSGR	430	440	450	460	470	480
a794.pep	AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX	490	500	510			
m794	AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

g900.seq

```
1 ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51 ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TGCGCGcctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TGC GTTGTGAT CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGGTG ATTTTCGCCG CCGAAAGTTT TTTCCGCTCG
251 CCCCAAGCCA AGCCGTCGGC AAGCAATTGC GTAATATCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGT TT TTTGTCTGTT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagt tCTTGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcg cATTTCgacg tgttgGATT GGTGCGCGCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCCG CATTTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCGCCT GGGTAATCAT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tGGGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGCGG AGGAAGAGGA
951 AGGATTCCGT ATCGGGGTTT TGCGCCGCGC GGACGGCGGG GCGGATGGCG
1001 CCGACGTTAGT TGCCCGAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCTTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA . gatgcgCCGA TTATACCCGA TTTGCCACAT ACATCCAGCC
1151 GacaACagac TTTTCCATAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

g900.pep

1	MPSEMPSETW	QAEVRTALGL	FORADADRIA	YFIQQFARFF	ARFLRACLQN
51	LFDLRRIRGQ	CVVAFAQFCQ	FGVDFRRRK	FRLAPSQAVG	KHLRKFRFR
101	RRGEGFIDFK	QRAFVGLFRL	ARLFHVGNDF	VDRFLGFFV	FPKRNGIAVG
151	FGHFASVQTD	QEFDFVDFDH	FGQGEEFLET	VGEAAGNVAR	HFDVLDLVAP
201	DGDFVGVEHQ	NVGSHQNRIT	EQTHFHTEIG	VFLPVFRIGL	NGGFVGVGAV
251	HQTLGGDAQ	NPVQLHHFNT	VALAVEGGAL	GVESAGKPSS	GNGLGGLVNH
301	<u>LLLVAFD</u> DAV	<u>VIGEEEE</u> GFG	IGVLRRADGG	ADGSAVVAQM	RAGAGGYAGQ
351	NSFFAHKNVL	TAAMPSEREK	DAPIIPDLPH	TSSRQOTFPY	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

```
1 ATGCCGCTCTG AAACGCGGCA GCGGAGGTT CGGACGGCAT CGGGTTCATT
51 TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG
```

```

151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CGGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTCGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGG GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFORA DADRIXFYVQ *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPRK NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFORADADRIGYFVQXFACFFTRFRRAACLQNLFDLRRVGGQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEFVDFKQWAFVGLFRL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      CVVAFQAQFCQFGVDFFRRKFFRLAPSAVGKHLRKFRRFRRRGEFGFIDFKQRAVGLFRL
          70      80      90     100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEEFPEA
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFASVQTDQEFVDFVDFHFGQGEEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFTEIRVFLPVFCICL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      VGEAAGNVARHFDVLDLVAPDGDVFGVEHQNVGSHQNRITEQTHFTEIGVFLPVFRIGL
          190     200     210     220     230     240

```

1283

	240	250	260	270	280	290
m900.pep	HGGFVGMGAHVHQTLSGDAQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	: : : : : :					
g900	NGGFVGVGAHVHQTLSGDAQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVIGEEEEFGFIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL					
	: : : : :					
g900	LLLVAFFDDAVVIGEEEEFGFIEVLRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360
	360	370	380			
m900.pep	AASMPSEREKDVPIIPDLPTSSRQQTFPYX					
	: : : : :					
g900	TAAMPSEREKDAPIIPDLPTSSRQQTFPYX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

1	GAGGTTCCGA	CGGCATTGGG	TTTATTTCAA	CGGGCGGATA	CCGACCGCAT
51	CACGTACTTT	GCCCAATAAT	TCGCGTGCTT	CTTTACGCGC	TTTTTGCGCG
101	CCTGCCTGCA	AAATCTCTTC	GATTTGCGAA	GGGTCGGCGG	TCAGCTCGTT
151	GTAGCGTTTCG	CGCGGTTCCG	CGAGTTCGGC	GTTGATTTTC	GCCGCCAAAA
201	GTTTTTTTGC	CTCGCCCCAA	GCCAAGCCGT	CGGCAAGCAT	TTTCGTAAAT
251	TCTGCCGTTT	CAGACGGCGT	GGAGAAAGCT	TTGTAGATTT	CAAACAGAGG
301	GCTTTCGTCG	GGCTTCTTCG	GCTCGCCCGG	CTCTTTCATA	TTGGTGATGA
351	TTTTGTTGAC	CGATTTTGGG	GTTTTTTTGT	CGTTTTTCCA	AAGCGGAATG
401	GTGTTGCCGT	AGGATTTGGA	CATTTTGCGT	CCGTCCAAAC	CAACCAAGAG
451	TTGACGTTT	TCGTCGATTT	TCACTTCGGG	CAGTGTGAAG	AGTTCCCGBA
501	AGCGGTGGTT	GAAGCGGCCG	GCAATATCGC	GTGCCATTTC	AACGTGTTGG
551	ATTTGGTTCG	GACCGACTGG	AACTTCATGG	GCATTGAACA	TGAGAATGTC
601	GGCAGTCATG	AGGATAGGGT	AGCTGTACAA	ACCCATTTC	ACGCCGAAAT
651	CGGGGTCTTC	CTGCCCGTTT	TCCGCATTTG	CCTGCACGGC	GGCTTTGTAG
701	GCGTGGGCGC	GGTTCATCAA	ACCCTTGCGC	GTGATGCAGG	TCAGAAATCCA
751	GTTCAATTCC	ATCACTTCGG	GAATGTCGCT	TTGACGGTAG	AAGGTGGTGC
801	GCTCGGGGTC	GAGTCCGCAG	GCAAGCCAAG	TGGCGGCAAC	GGCTTGGGTG
851	GATTGGTGAA	TCATCTCCGG	CTCGTGGCAT	TTGATGATAC	CGTGGTAATC
901	GGCGAGGAAG	AGGAAGGATT	CGGTATCAGG	GTTTTGCGCC	GCGCGGACGG
951	CGGGGCGGAT	AGCACCGACG	TAGTTGCCCA	GATCGGGGAT	GCCGGTGGTG
1001	GTTACGCCGG	TCAGAACTCG	TTTTTTGCTC	ATAAAAATGT	CCTTGCGGCA
1051	TCAATGCCGT	CTGAAAGGGA	AAAAGATGCG	CCGATTATAC	CCGATTTGCC
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAA	

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

1	EVRTALGLFQ	RADTDRTITYF	AQ*FACFFTR	FLRACLQNL	DLRRVGGQLV
51	VAFAFGEFG	VDERRQKFFC	LAPSOAVGKH	FRKFCRFR	GESFVDFKQR
101	AFVGLRLAR	LFHIGDDFVD	RFLGFFVFP	KRNGVAVGFG	HFASVQTNQE
151	FDVFVDFHFG	QCEEFPEAVV	EAAGNIACHF	NVLDLVATDW	NFMGIEHENV
201	GSHEDRVAVQ	THFHAIEIGVF	LPVFRICLHG	GFVGVGAHVQ	TLGGDAQNP
251	VQFHHFGNVA	LTVEGGALGV	ESAGKPSGGN	GLGGLVNH	LVAFDDTVVI
301	EEEEEGFIR	VLRRADGGAD	STDVVAQMRD	AGGGYAGQNS	FFAHKNVLA
351	SMPSEREKDA	PIIPDLPTS	SRQQTFFPY*		

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFRFRACLQNLFDLRRVGGQLVVA					
	: : : : :					
a900	EVRTALGLFQADTDRTITYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

```

m900.pep      FARFGFEGVDFFRRQKFFGGFTPRQAVGKHFRRKFFRRRRGEGFVDFKQWAFVGLFRLARLF
a900          |||||::| ||||| |||||:|||||:|||||
              60      70      80      90      100     110

m900.pep      HIGDDFVDRLGFFVVFPPKRVAVGVFGHFASVQTDQEFVDFIDFHFGQGEFFPEAVVEA
a900          ||||| ||||| ||||| ||||| |||||:|||||:||||| ||||| |||||
              120     130     140     150     160     170

m900.pep      AGDVARHFDVLDLVPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
a900          ||||| ||||| ||||| ||||| |||||:|||||:||||| ||||| |||||
              180     190     200     210     220     230

m900.pep      VGMGAHVQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHRLRV
a900          ||||| ||||| ||||| ||||| |||||:|||||:||||| ||||| |||||
              240     250     260     270     280     290

m900.pep      AFDDTVVIGEEEEGGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
a900          ||||| ||||| ||||| ||||| |||||:|||||:||||| ||||| |||||
              300     310     320     330     340     350

m900.pep      PSEREKDVPIIPDLPTSSRQQTFFPYX
a900          |||||:||||| ||||| ||||| |||||
              360     370

```

```
g901.seq    not found yet
g901.pep    not found yet
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

m901.seq

```
1 ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT
51 GGTGCCCGGT TTGTTTACCG TATTakGyAG TGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGTTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAATTT CCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGTATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCACCC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGGG
601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGCCCA TGAAACCGTT
751 TACGGCTGTA CAACGGGTAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTTTA
```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

m901.pep

1	MPDFSMSNLA	VAFSITLAAG	LFTVLXSGLV	MFSKTPNPRV	LSFGLAFAGG
51	AMVYVSLTEI	FSKSSEAEAE	IYDKDHAFAA	ATMAFLAGMG	GIALIDRLVP

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCGATT TTTGATGTC CAATTTGGCC GTTGCTTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
 251 CATTTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
 401 CGCACAAATTT CCCCAGAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAT
 451 CCAGCAGTCG GGATGCCCTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCACC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGCCCGA GCCGTTGGGG
 601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
 701 ACGAGCTGCT GCCGCGTGCC AAACGCTATT CAGACGGCCA TGAACCGTT
 751 TACGGCCTGA CAATGGGCAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFMSNLA VAFSITLAAG LFTVLXSG LVMFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	10	20	30	40	50	60
	MPDFMSNLA VAFSITLAAG LFTVLGSG LVMFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
m901.pep	70	80	90	100	110	120
	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVNPHE TLDAQDPSFQESKRRH					
a901	70	80	90	100	110	120
	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVNPHE TLDAQDPSFQESKRRH					
m901.pep	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLENPAVGMPLALAIAIHNIPEGISIAAPVYFAT					
a901	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLENPAVGMPLALAIAIHNIPEGISIAAPVYFAT					
m901.pep	190	200	210	220	230	240
	RSRKKTWAC LLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELLPAA					
a901	190	200	210	220	230	240
	RSRKKTWAC LLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELLPAA					
m901.pep	250	260	270			
	KRYSDGHETVYGLTTGMAVIAVSLVLFHFX					
a901	250	260	270			
	KRYSDGHETVYGLTMGMAVIAVSLVLFHFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```
1 ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51 GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTGCGCGT CCGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCGATG
251 GCGCGGATGT GGTTCAAAAT GCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTTCAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgcG CGcgcccgtg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcgG gcagggtttg
601 atcgtcgtcg tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcg
801 catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```
1 MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51 TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAAI F GDFGDDGQVL
201 IVVVPQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDL RPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQFGSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```
1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51 CGCACGCCCA ACTGTGCGGT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTTC CCGTcGGGCA TTTCTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTGCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTGCGCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTTC TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTGCGCGAT TTTGGCGATG ACGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCGCCGAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTGCGTAA TGCCCCCAT CCGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTCAAAAAA GTACGCCATT GTACATTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLR	RTVQAVDFTT
51	CLFAVGHFVD	VPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFCQTQGR
101	QNTVFGIMFQ	IAEPRPALR	AAPYHNAVGG	GLFEDGLGFL	RRSNVAVDPD
151	RDVQTAFGFG	DEFVTRFAFV	HLRTRASVDG	KGGDAAIFGD	FGDDGQVLMV
201	VVPTQTGFEG	NGYACRTDDG	FQNGGNQRLV	LHQRTGLDI	ADFFSGTAHV
251	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA	VQGFSSISER
301	RVAGQHFHAHR	PTCAKISAKS	AERFVGNARH	RRKCDGVVDK	IAADVHNGSA
351	FQKSTPLYIF	*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

		10	20	30	40	50	
m902.pep		LHFQRI	IKCEGIWAVGARPTVGFFGKSFKITCKHVVLR	RRRTVQAVDFTTCLFAVGHF			
			:	:			
g902		MPSEPERRHGNTALPFP	PIAARPTVGFS	GKPFKITGKCVVLR	RRRIVQAVDFT	TPRLFAVGHF	
		10	20	30	40	50	60
	60	70	80	90	100	110	
m902.pep		VDVPAYVFACDAHTGGVAVKRVYGADV	VQNSGGAF	CQTQGR	RQNTVFGIM	FQIAEEPRPA	
	:						
g902		ADV	PAYVFACDAHTDGLTIKRVHGADV	VQNGGS	AF	CQTQGR	RXNAVFGIMLQIAEKPRPA
		70	80	90	100	110	120
	120	130	140	150	160	170	
m902.pep		LRAAPYHNAVGGGLFEDGLGFLRRSNVAVD	PDRD	VQTA	FGFGDEFV	TRFAFVHLR	TRASV
g902		LRAAPYHDAVGGGLFEDGGGFLRRSDVAVD	PGRD	VQTA	FGGLGDEFV	TRLAFVHLR	ARAPV
		130	140	150	160	170	180
	180	190	200	210	220	230	
m902.pep		DGKGGDA	AI	FGDFGDDGQVLMVVVPTQTGF	EGNGYACRTDDG	FQNGGNQRLVLHQR	ATGL
	:						
g902		NGKGGNA	AI	FGDFGDDGQVLIVVVPTQTGF	EGNGYARRLDHRLQNGGNQRLVLHQR	ATGL	
		190	200	210	220	230	240
	240	250	260	270	280	290	
m902.pep		DIADFFSGTAHV	DVDKLRPKADV	TRGIRHLLRIASGNLHG	NNAAFI	GKIAAVQGF	SSIS
g902		DVAHFLGGA	AHIDVDDL	RPESDVVTRRIRHLFGVAAGNLHG	NDAAFI	GKITAVQGF	SGIP
		250	260	270	280	290	300
	300	310	320	330	340	350	
m902.pep		ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDG	VVDKIAADVHNGSAFQKSTPLY				
g902		ERRIAGQHFAHRPTCAKRPTEAAEGFVGNARHRRKCDG	VVDKITADVHNGPAFQKSAPLY				
		310	320	330	340	350	360
	360						
m902.pep		IFX					
g902		IFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51 CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTC AAG ATAACCTGCA

```
101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAACACCGG TGTTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAAGGT AACGGGTACG CCCGCCGCTT
651 TGACCAACCGC CTCCAAATG CGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFQCQTQRR
101 *NTVFGVMFQ IAEEPRSAIR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFFG NGVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARREFDH LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *
```

m902/a902 94.7% identity in 360 aa overlap

m902.pep	10	20	30	40	50	60
	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLRR	RTVQAVDFTT	CLFAVGHFVD
a902	10	20	30	40	50	60
	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLRR	RTVQAVDFTT	CLFAVGHFVD
m902.pep	70	80	90	100	110	120
	VPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFQCQTQ	RRQNTVFG	IMFQIAEE
a902	70	80	90	100	110	120
	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNS	GGTFCQTQ	RRXNTVFG	VMFQIAEE
m902.pep	130	140	150	160	170	180
	AAPYHNAVGG	GLFEDGLG	FLRRSNVAV	DPDRDVQTA	FGFGDEFV	TRFAFVHL
a902	130	140	150	160	170	180
	AAPYHNAVCG	GLFEDGLG	FLRRSNVAV	DPDRDVQTA	FGFGNQVVS	RFAFVHLR
m902.pep	190	200	210	220	230	240
	KGGDAAFGD	FGDDGQV	LMVVPTQT	GFEGNGYAC	RDDGFGQ	NGGNQRLV
a902	190	200	210	220	230	240
	KGGNAAFGD	FGDDGQV	LMVVPTQT	GFEGNGYAR	RFDHRLQ	NGGNQRLV
m902.pep	250	260	270	280	290	300
	ADFFSGTAH	VDVDKLR	PKADVVT	RGIRHLLR	IASGNLHG	NNAAFIGK
a902	250	260	270	280	290	300
	ADFFSGTAH	VDVDKLR	PKADVVT	RGIRHLLR	IASGNLHG	NNAAFIGK
m902.pep	310	320	330	340	350	360
	RVAGQHFAH	RPTCAKIS	AKSAERFV	GNARHRR	KCDGVVDK	IAADVHNG
a902	310	320	330	340	350	360
	RVAGQHFAH	RPTCAKIS	AKSAERFV	GNARHRR	KCDGVVDK	IAADVHNG

```

a902      |||||
          RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep   X
            |
a902        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattc gatgaggCAA GCCCTGCTT
51 TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCCTTcaa ccaTGCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TCtgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTG GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTTCG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRs
101 IRIDRSNDDQ THAGRIAAFG NKFPTRSNL LNLRLLEOGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVQ WRXRLLPYCV SVGMDSNGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKSIIIDAEI TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTFPQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGWS WRNDLSWQFK
451 PGHQLYLGAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKVVTFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51 CCGTTTCGAG CAACATTGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```

```

151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCCTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCACT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTTCATATG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAAGT TACAGCGTGC ATTATTCCGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACCTCA GTCGGAATGA AATTATGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGCTTTAC AAACCGCGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATT C AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGCA AGCCGCTTCA TAAACCAAAA GGCTTTTACA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEERKRDG KSAEGSISAF NKNFPLYRKN
151 ILNLRDVEQG LENLRLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFVVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          |:::| |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
          10      20      30

          70      80      90      100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI QPQNMDSGIL KLRVSAGEIG
          : : | | : | | : : : : : : : : : : : : : : : :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKLQTLMPGYLR
          40      50      60      70      80      90

```

1291

	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLNLRRLPSVKTDIQIIPSE					
g903	SIRIDRSNDDQTHAGRIAFAFQNKFPTRSNDDLNLRLDLEQGLNLRKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQNK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDFVYSYGR					
g903	REPNSQSDVVVQWRXLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFVYNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLTDTGTETESGSRYSVHYSPVKKWLFSFNHNGHRYHEATEGYSVNYDYNG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSGVMKLTROTQYKYIDDAEIEVQRRRSAGWEAELRHRAY					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDDAELTVQRRKTTGWLAEELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQOFF					
g903	IGRSTADFKLYKHGTGMKDALARPEEAFGE--GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAERGWWYWRNDLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAGTAIGIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
g903	TGFQVGYSEFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACTGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTC	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TGGGAAAACC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT

1292

```
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAG CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCCGGT
801 GCCCCGTAATA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```
1 MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NKFPLYRKN
151 IILNLRDVEQG LENLRLRPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYVSVVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ
301 YQSSLAERM LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRLAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAAPF MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

m903/a903 98.4% identity in 547 aa overlap

```
10 20 30 40 50 60
m903.pep MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
a903 MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTARKFSFLPSVL
10 20 30 40 50 60
70 80 90 100 110 120
m903.pep MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
a903 MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
70 80 90 100 110 120
130 140 150 160 170 180
m903.pep DIRYEEKRDG KSAEGSISAF NKFPLYRKN IILNLRDVEQG LENLRLRPSV KTDIQIIPSE
a903 DIRYEEKRDG KSAEGSISAF NKFPLYRKN IILNLRDVEQG LENLRLRPSV KTDIQIIPSE
130 140 150 160 170 180
190 200 210 220 230 240
m903.pep EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL
a903 EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL
190 200 210 220 230 240
250 260 270 280 290 300
m903.pep AHKTDLT DATGTETESGSR SYSVHYVSVVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ
a903 VHKTDLT DATGTETESGSR SYSVHYVSVVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ
```

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSGVMKLTWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRLAYLN					
a903	YQSSLAERMLWRNRFHKTSGVMKLTWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRLAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQOFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDITPGTSRMKIITAGLDAAAPFMLGKQOFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCGAGCT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATAACGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCGACC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCCGA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTTCGTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CTTTGCCGCG GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatattA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRRFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

```

51  AGHGFVNRF  GFHRIARTARQ  DVGFAAAWQF  VADADIDGFN  AVHYIEFGNA
101 HTGNAVLDLG  AFQGGGKPA  AAARAAGYRT  EFVSALRQTC  AYFVEQFGRE
151 RARTDARGIG  FDDAQNIQH  LRTYARACRS  RAGETVGRGN  EGVSAVVDVQ
201 QRTLRAFQKQ  FFAVFVFFVQ  HAGHVGNHRR  NARRDFFDNR  HHVFRFNRSR
251 VMQVLELDV  IGKDGIFFT  QFFRMQIGG  ANGAACHFVF  VGRADAAAGR
301 ADFAFAARCF  AGLVERDVVR  QDQAGRRDF  QTAFDVFHAC  RVQLVDFAQQ
351 GFGGNDNART  DEAIQSFVQD  TARNQAQNGF  FAADDQGMAR  IVAALEAHDA
401 AGFRQPVND  FTFTLVAPLC  ADYINIFSHS  HITRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

m904.seq

```

1  ATGATGCAGC  ACAATCGTTT  CTTCTCGGTC  GGGGCCGgTG  GAGACGATGG
51  CGACCGGCGC  GCCGCAGACT  TCTTCAATCC  GTTTCAAATA  TGCTTTGGCG
101 TTTTCGGGCA  ATGCGCCGTA  GTCCTTCACG  CCGAAAGTGG  ATTCGCGCCA
151 GCCGGGCATG  GTTTCGTAAA  TCGGCTTGCA  GGTTCACCAC  GCATCGGAAC
201 CGCAAGGCAG  GATGTCGGTT  TTGCCGCCGT  CGGGCAATTC  ATAGCCGACG
251 CAGATATTGA  TGGTTTCAAC  GCCGTCCATT  ACATCGAGTT  TAGTAATACA
301 CATACCGGAA  ATGCCGTTGA  TTTGGATGGA  GCGTTTCAGG  GCGGCGGCAT
351 CAAACCAGCC  GCAGCGGCGT  GCGCGTCCGG  TTACCGAACC  GAATTCTGTG
401 CCGCGTCTTG  CCAAACCTAC  GCCTACTTCG  TCGAACCAAT  CGGTCGGGAA
451 CGGGCCCCGA  CCGACGCGCG  TGGTATAGGC  TTTGACGATG  CCAAAACAT
501 AATCCAGCAT  TTGAGGACCT  ACGCCCGCGC  CTGCCGAAGC  TCGCCCCGCC
551 AGACAGTTGG  ACGAGGTAAC  GAAGGGATAA  GTGCCGTAGT  CGATGTCCAA
601 CAACGCACCT  TGCAGCGCCT  CAAACAGCAG  TTTTTCGCCG  TTTTGTGTTT
651 TCTCGTTCAA  CACGCGGGAC  ACGTCGGTAA  TCATCGGCGC  AATGCGCGGC
701 GCGACTTTTT  CGATAACCGC  CATCACGTCT  TCCGCTTTAA  CCGGCTCGGC
751 ATTGTGCAGA  TGTTCAGTT  GGACATTGTA  ATAGGCAAGG  ACGGCATCCA
801 GTTTTTTCAG  CAGTTTCTCA  GGATGCAGCA  AATCGGCGGC  GCGAATGGCG
851 CGGCGTGCCA  CTTTGTCTTC  GTAGGCAGGG  CCGATGCCGC  GGCCGTCGT
901 GCCGATTTTG  CCTTGCCGC  GCG.ATcTTC  GCGGCTTGG  TCGAGCGCGA
951 TGTGGTAAGG  CAGGATCAGC  GGGCAGGTCG  GCGCGATTTT  CAGACGGCCT
1001 TCGACGTTTT  TCACGCCTGC  CCGCTTCAAC  TCGTCGATTT  CGCCCAACAG
1051 GGCTTCGGGG  GAGACGACAA  CGCCGAACC  GATGAAGCAG  TCCAACTTT
1101 CATGCAGGAT  GCCGCTCGGA  ATCAGGCGCA  AAATGGTTTT  TTTGCCCGCG
1151 ACAACCAAGG  TATGGCCCGC  ATTGTGGCCG  CCTTGAAGC  GCACCaCGCC
1201 GCCGGCTTCT  TCCGCCAGCC  AGTCAACGAT  TTTACCTTTA  CCCTCGTCGC
1251 CCCACTGTGC  GCCGATTAsT  ACAACATTTT  TAGCCATAGC  CATATAACCT
1301 ATCGATATTA  A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904.pep

```

1  MMQHNRF  GAGGDDGDRR  AADFFNPFI  CFGVFGQCAV  VLHAESGFAP
51  AGHGFVNRL  GFHRIGTARQ  DVGFAAVGQF  IADADIDGFN  AVHYIEFSNT
101 HTGNAVLDLG  AFQGGGKPA  AAACASGYRT  EFVSALRQTC  AYFVEQFGRE
151 RARTDARGIG  FDDAQNIQH  LRTYARACRS  CARQTVGRGN  EGISAVVDVQ
201 QRTLRAFQKQ  FFAVFVFLVQ  HAGHVGNHRR  NARRDFFDNR  HHVFRFNRLG
251 IVQMLQLDIV  IGKDGIFFT  QFXRMQIGG  ANGAACHFVF  VGRADAAAGR
301 ADFAFAAXIF  AGLVERDVVR  QDQAGRRDF  QTAFDVFHAC  RVQLVDFAQQ
351 GFGGDDNART  DEAVQTFMQD  AARNQAQNGF  FAADNQGMR  IVAALEAHHA
401 AGFRQPVND  FTFTLVAPLC  ADXYNIFSHS  HITRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

```

          10      20      30      40      50      60
m904.pep  MMQHNRF  SVGAGGDDGDRRAADFFNPFI  CFGVFGQCAVVLHAESGFAPAGHGFVNRLA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904      MMQHNRF  FAVGAGGDDGDRRAADFFNPFI  CFGIGRQCVVAFHADS RFAPAGHGFVNRLA
          10      20      30      40      50      60
          70      80      90     100     110     120

```


1295

m904 . pep	GFHRIGTARQDVGF	AAVGGQFIADADIDGF	NAVHYIEFSNTH	TGNAVDLDGAF	QGGGIKPA
g904	GFHRIRTARQDVGF	AAAWQFVADADIDGF	NAVHYIEFGNAHT	TGNAVDLDGAF	QGGGIKPA
	70	80	90	100	110 120
m904 . pep	AAACASGYRTEFVS	AFCQTYAYFVEQFGR	ERARTDARGIGFDD	AQNI IQHLRTYAR	ACRS
g904	AAARAAGYRTEFVS	ALRQTCAYFVEQFGR	ERARTDARGIGFDD	AQNI IQHLRTYAR	ACRS
	130	140	150	160	170 180
m904 . pep	CARQTVGRGNEGIS	AVVDVQORTLRAF	KQQFFAVFVFLVQ	HAGHVGNHRRNARR	DFDNR
g904	RAGETVGRGNEGVS	AVVDVQORTLRAF	KQQFFAVFVFFVQ	HAGHVGNHRRNARR	DFDNR
	190	200	210	220	230 240
m904 . pep	HHVFRFNRLGIVQ	MLQLDIVIGKDG	IQFFTFXRMQQIG	GANGAACHFV	FVGRADAAAGR
g904	HHVFRFNRS	GVMMQVLELDV	VIGKDG IQFFTF	FRMQQIGGANGA	ACHFVGRADAAAGR
	250	260	270	280	290 300
m904 . pep	ADFAFAARIFAGL	VERDVVRQDORAGR	RRDFQTA	FDVFHACRVQLV	DFAQQGFGGDDNART
g904	ADFAFAARCFAGL	VERDVVRQDORAGR	RRDFQTA	FDVFHACRVQLV	DFAQQGFGGNDNART
	310	320	330	340	350 360
m904 . pep	DEAVQTFMQDAARN	QAQNGFFAADNQGM	ARIVAAL	EAHHAAGFFRQ	PVNDFTFTLVAPLC
g904	DEAIQSFVQDTARN	QAQNGFFAADNQGM	ARIVAAL	EAHDAAGFFRQ	PVNDFTFTLVAPLC
	370	380	390	400	410 420
m904 . pep	ADXYNIFSHSHIT	YRYX			
g904	ADYYNIFSHSHIT	YRYX			
	430				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

```

1  ATGATGCAGC ACAATCGTTT CTTGCGGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTCTTG CCAAACCTGC TCCGACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGGCCT ACGCCCGCGC CTGCCGAAGC CGCGCCGCG
551 AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTTTT
651 TTTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGT AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTTCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CTTTGCCGC GCGATGCTTC TCGGCTTG TCGAGCGCGA

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1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904 .pep

```

1 MMQHNRRFFAV GAGGDDGDRR TADFFNPFI CFIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRAAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFKQQ FFAVFVFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQIGG ANGAACHEVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYNNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904 .pep	10	20	30	40	50	60
	MMQHNRRFFSVGAGGDDGDRRAADFFNPFI	CFI	GR	*CVV	AFHAESGFAPAGHGFVNRLA	
a904	MMQHNRRFFAVGAGGDDGDRRTADFFNPFI	CFI	GR	XCVVAFHAESGFAPTGHGFVNRLA		
	10	20	30	40	50	60
m904 .pep	70	80	90	100	110	120
	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTH	TGN	AVDLDGAFQGGGIKPA			
a904	GFYRIRAAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTH	TGN	AVDLDGAFQGGGIKPA			
	70	80	90	100	110	120
m904 .pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQH	LRTYARACRS				
a904	AAACASGYRTEFVSAFCQTCSDFVEQFGRERARTDARGIGFDDAQNIQH	LRTYARACRS				
	130	140	150	160	170	180
m904 .pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQORTLRAFKQQFFAVFVFLVQHAGHVGNNRR	NARRDFFDNR				
a904	RAGEAVGRSNEGVS	AVVDVQORTLRAFKQQFFAVFVFLVQHAGHVGNNRR	NARRDFFDNR			
	190	200	210	220	230	240
m904 .pep	250	260	270	280	290	300
	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQIGGANGAACHFV	FVGRADAAAGR				
a904	HHVFRFHRLGIVQMLQLDVVISKDGIOFFTQFFRMQIGGANGAACHFV	FVGRADAAAGR				
	250	260	270	280	290	300
m904 .pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFAQQ	GFGGDDNART				
a904	ADFAFAARCFSGLVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFAQQ	GFGGDDNART				
	310	320	330	340	350	360
m904 .pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVND	FTFTLVAPLC				
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVND	FTFTLVAPLC				
	370	380	390	400	410	420

430

```

m904.pep    ADXYNIFSHSHITYRYX
             || ||||| ||||| |||
a904        ADYYNIFSHSHITXRYX
             430

```

g906.seq not found yet

g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
  1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101  TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151  CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201  CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251  GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAACAAA
301  AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
  1  MKYIVSISLA MGLAACSFEGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101  KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
  1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
 51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101  CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151  TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201  GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCTGTC
251  CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301  AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351  aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
  1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
 51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101  SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
  1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
 51  GTTGTGTGCC GCCGGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101  CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151  TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201  GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCTGTC
251  CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301  AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351  AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGCGCTGA
401  TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAACC GGCGCACAAc
451  CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501  TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551  ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601  CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
  1  MRKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
 51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101  SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW KNYIGKPAHN

```

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	:	:	:	:	:	:
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
g907.pep	RARIIS					
m907	ROYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

1	ATGAAAAAAC	CGACCGATAC	CCTACCCGTC	AATCTGCAAC	GCCGCCGCCT
51	ATTGTGTGCT	GCCGGCGCGC	TGTTGCTCAG	CCCGCTGGCA	CAAGCCGGCG
101	CGCAACGTGA	AGAAACGCTT	GCCGACGATG	TGGCTTCCGT	GATGAGGAGC
151	TCTGTGCGCA	GCATAAATCC	GCCGAGGCTG	GTGTTCGACA	ATCCGAAAGA
201	GGGCGAGCGT	TGGCTGTCCG	CGATGTCTGC	TCGGTTGGCA	AGGTTCTGTC
251	CCGATGAGGA	GGAGCGGCGC	AGGCTGCTGG	TCAATATCCA	GTACGAAAGC
301	AGCCGGGCGG	GTTTGGATAC	GCAGATTGTG	TTGGGGCTGA	TTGAGGTGGA
351	AAGCGCGTTC	CGCCAGTATG	CAATCAGCGG	TGTCGGCGCG	CGCGGCCTGA
401	TGCAGGTTAT	GCCGTTTTGG	AAAAACTACA	TCGGCAAACC	GGCGCACAAAC
451	CTGTTTCGACA	TCCGCACCAA	CCTGCGTTAC	GGCTGTACCA	TCCTGCGCCA
501	TTACCGGAAT	CTTGAAAAAG	GCAACATCGT	CCGCGCACTC	GCCCCTTTTA
551	ACGGTAGCCT	CGGCAGCAAT	AAATATCCGA	ACGCCGTTTT	GGGCGCGTGG
601	CGCAACCGCT	GGCAGTGGCG	TTGA		

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

1	MKKPTDTLPV	NLQRRRLCA	AGALLSPLA	QAGAOREETL	ADDVASVMRS
51	SVGSINPRL	VFDNPKEGER	WLSAMSARLA	RFVPDEEERR	RLLVNIQYES
101	SRAGLDTQIV	LGLIEVESAF	ROYAISGVGA	RGLMQVMPFW	KNYIGKPAHN
151	LFDIRTNLRY	GCTILRHYRN	LEKGNIVRAL	ARFNGSLGSN	KYPNAVLGAW
201	RNRWQWR*				

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAOREETLADDVASVMRSSVGSINPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	:	:	:	:	:	:
a907	VFDNPKEGERWLSAMSARLARFVPEDEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

1299

	70	80	90	100	110	120
m907.pep	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
a907	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
m907.pep	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPIIREQVK PDSIVYTDCY RSYDVLVDVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGCG AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSQYK QXKLIELFVT GVTARTAAEL VGVNKNNTAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPIIREQVK PDSIFYTDCY RSYDVLVDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g908.pep	MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMF					

```
m908      | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNATAAYYFHLRLLLIYQNSPHLEMFD  
          10           20           30           40           50           60  
  
          70           80           90          100          110          120  
g908.pep  GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLPFIIREQVK  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
m908      GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLPFIIREQVK  
          70           80           90          100          110          120  
  
          130          140          150          160  
g908.pep  PDSIVYTDCYRSYDVLDVSEFSHFSAETSFSYSQSHTFCRTTKPYX  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
m908      PDSIFYTDCYRSYDVLDVREFSHFSAETSFSYSQSHTFCRTTKPYX  
          130          140          150          160
```

1	ATGAGAAAAA	GTCGTCTAAG	CCAGTATAAA	CAAAATAAAC	TCATTGAGCT
51	ATTTGTCGCA	GGTGTAACTG	CAAGAACGGC	AGCAGAGTTA	TAGGCGGTTA
101	ATAAAAATAC	CGCAGCCTAT	TATTTTCATC	GTTTACGATT	ACTTATTTAT
151	CAAAACAGTC	CGCATTTGGA	AATGTTTGAT	GGCGAAGTAG	AAGCAGATGA
201	AAGTTATTTT	GGCGGACAAC	GCAAAGGCAA	ACGCGGTGCG	GGTGCTGCCG
251	GTAAAGTCGC	CGTATTCGGT	CTTTTGAAGC	GAATGGTGA	GGTTTATACG
301	GTTACAGTAC	CGAATACTCA	AACCGCTACT	TTATTTCTTA	TTATCCGTGA
351	ACAAGTGAAA	CCTGACAGCA	TTGTTTATAC	GGATTGTTAT	CGTAGCTATG
401	ATGTATTAGA	TGTGCGCGAA	TTTAGCCATT	TTAGCTTCGC	TGAAACTTCG
451	TTTTCGTATC	AATCACAGCA	CACATTTTGC	CGAACGACAA	AACCATATTA
501	A				

1 MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51 QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPPIREQVK PDSIVYTCY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

m908.pep      10      20      30      40      50      60
MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAYYFHLRLLLIYQNSPHLEMFD
|||||:|||||
a908          10      20      30      40      50      60
MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNTAAYYFHLRLLLIYQNSPHLEMFD

m908.pep      70      80      90      100     110     120
GEVEADESYFGGQQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFPIIREQVK
|||||
a908          70      80      90      100     110     120
GEVEADESYFGGQQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFPIIREQVK

m908.pep      130     140     150     160
PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
|||||
a908          130     140     150     160
PDSIVYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX

```

```

1  atgcgtaaaa  ccgtacttat  cCTgaccatc  tccgccgccc  ttttgtcggg
51  ctgcacatgG  gaaactttatc  aagacggcag  cggcaaaacc  gccgtccgtg
101  caaaatgttc  caccggcacg  ccgctgtgtt  ggcaagacgg  gcgcggctcg

```

1301

151 aaaaagggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
 201 caacccaaaag cgggggaagc ccgacgagag gagagccgca acgctgggga
 251 aaccgagttt ccgggagagg gacggggggg ggcgggtgaa cagggcagaa
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEKRSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTTGTGCGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAAAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	SKKVDCDEYGG
	10	20	30	40	50	60

	70	80	90
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNRX
	:		: : :
g909	ERRAVLRNQK	RGKPTRRAA	TLGKPSFRARDGGGRVNRAETGEGKRSAR
	70	80	90 100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTTGTGCGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFILIMT AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
a909	MRKTFILIMT	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

g910.seq

1	ATGAAAAAAC	TGTTATTGGC	CGCCGTTGTT	TCCCTAAATG	CCGCAACCGC
51	ATTTGCCGGC	GACTCTGCCG	AGCGTCAGAT	TTACGGCGAT	CCCCATTTTG
101	AACAAAACCG	CACAAAAGCC	GTGAAAATGT	TGGAACAGCG	CGGTTATCAG
151	GTTTACGATG	TCGATGCCGA	CGACTACTGG	GGCAAACCTG	TTTGGGAAGT
201	GGAAGCCTAT	AAAGACGGCC	GCGAATACGA	CATCGTGTG	TCTTACCCCG
251	ACCTGAAAAT	CATCAAAGAG	CAGCTCGATC	GCTGA	

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

g910.pep

1	MKKLLLLAAVV	SLNAATAFAG	DSAERQIYGD	PHFEQNRTKA	VKMLEQRGYQ
51	VYDVDADDYW	GKPVLEVEAY	KDGREYDIVL	SYDDLKIIKE	QLDR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

m910.seq

1	ATGAAAAAAC	TGTTATTGGC	TGCCGTTGTT	TCTCTGAGTG	CCGCTGCCCGC
51	ATTTGCCGGC	GACTCTGCCG	AGCGTCAGAT	TTACGGCGAT	CCCCATTTTG
101	AACAAAACCG	CACAAAAGCT	GTGAAAATGT	TGGAGCAGCG	CGGTTATCAG
151	GTTTACGATG	TCGATGCCGA	CGACCATTGG	GGTAAGCCTG	TGCTGGAAGT
201	GGAAGCCTAT	AAAGACGGCC	GCGAATACGA	CATCGTGTG	TCTTACCCCG
251	ACCTGAAAAT	CATCAAAGAG	CAGCTCGATC	GCTGA	

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

m910.pep

1	MKKLLLLAAVV	SLSAAAFAG	DSAERQIYGD	PHFEQNRTKA	VKMLEQRGYQ
51	VYDVDADDDHW	GKPVLEVEAY	KDGREYDIVL	SYDDLKIIKE	QLDR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

g910/m910

	10	20	30	40	50	60
g910.pep	MKKLLLLAAVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW					
m910	MKKLLLLAAVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

a910.seq

1	ATGAAAAAAC	TGTTATTGGT	CGCCGTTGTT	TCCTTGAGTG	CCGCAACCGC
51	ATTTGCCGGC	GACTCTGCCG	AGCGTCAGAT	TTACGGCGAT	CCCTATTTTG
101	AACAAAACCG	CACAAAAGCC	GTGAAAATGT	TGGAACAGCG	CGGTTATCAG
151	GTTTACGATG	TCGATGCCGA	CGACCATTGG	GGCAAACCTG	TTTTGGAAGT
201	GGAAGCCTAT	AAAGACGGCC	GCGAATACGA	CATTGTGTG	TCTTACCCCG
251	ACCTGAAAAT	CATCAAAGAG	CAGCTCGATC	GCTGA	

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

a910.pep

1303

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
 51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAAFAG	DSAERQI	YGD	PYFEQNRTKAVKMLEQRGYQVYD
	:	:	:	:	:	:
a910	MKKLLLV	AVVSLS	AATAFAG	DSAERQI	YGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDDHW
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYKD	GREYDI	VL	SYPDLK	IIKEQLDRX
	:	:	:	:	:	:
a910	GKPVLE	VEAYKD	GREYDI	VL	SYPDLK	IIKEQLDRX
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
 1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCTTGATCGG
 51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCG CGTGGCGGGC GGCGCGGCGT
 101 TCGGCGGTTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTTCGG
 201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
 251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
 301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
 351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
 401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
 451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
 1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
 151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
 1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCCTGATTGG
 51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCG CGTGGCGGGC GGTGCGGCGT
 101 TCGGCGGTTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTTCGG
 201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
 251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
 301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
 351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
 401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTCGCC
 451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
 1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
 151 EKNAEGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGSDKTYAVYADFGDIGGLKVNAPVK
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGSDKTYAVYADFGDIGGLKVNAPVK
           10      20      30      40      50      60

           70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
m911      SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
           70      80      90      100     110     120

           130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEE
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEE
           130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
  1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCCTGATTGG
 51  CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCG CGTGGCCGCG GGTGCGGCGT
101  TCGGCGGTTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151  GGCGGTTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201  GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251  GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301  ATCCTGACTT CGGACTTTT GGGCAGCAG TACATCGGGC TGCAGCAGGG
351  CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
401  CTGCAATGGT TCTGGAACAC CTTATCGGCA AATTCATGAC GAGTTTGTCC
451  GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
  1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101  ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151  EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGSDKTYAVYADFGDIGGLKVNAPVK
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGSDKTYAVYADFGDIGGLKVNAPVK
           10      20      30      40      50      60

           70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
a911      SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
           70      80      90      100     110     120

           130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEE
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEE
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
  1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
 51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101  ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

151	CGCCCAAAAG	CCGAAGCCTA	TGCGGTTCCC	TATTTGATT	TCCAACGTAT
201	GACCGCATTG	GCGGTCGGCA	ACCCTTGGCG	TACCGCGTCC	GACGCGCAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCAGCATGC	TGAAATTCAA	AAACGCGACC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAGGGCGGCA	AGGAAATCGT	CGTCCGTGCC	GAAGTCGGCA
401	TCCCGGTCGA	GAAGCCCGTC	AATATGGACT	TTACCACCTA	CCAAAGCGGC
451	GGCAAATACC	GTACCTACAA	CGTCGCCATC	AAGGCACGA	GCCTGGTTAC
501	CGTGTACCGC	AACCAATTCT	GCGAAATCAT	CAAAGCCAAA	GGCATCGACG
551	GGCTGATTGC	CGAGTTGAAA	GCCAAAAACG	GCGGCAAATA	A

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

g912.pcp

1 VKKSSFISAL GIGILSIGMA FASPADAVGQ IRONATQVLT ILKSGDAASA
51 RPKAEAYAVP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTL LIR TYS
101 GTMLKFKNAT VNVKDNPIVN KGKKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI IKAK GIDGLIAELK AKNGGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

m912.seq

1	ATGAAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTTGAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CCGAAGCCTA	TGCGATTCCC	TATTTTCGATT	TCCAACGTAT
201	GACCCGATTG	CGGGTCGGCA	ACCTTGGCG	CACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAAGCGGC
451	GGTAAATACC	GTACCTATCA	CGTCGCCATC	GAAGGCGCGA	GCCTGGTTAC
501	CGTGTACCGC	AACCAATTAG	GCGAAATTAT	CAAAGCGAAA	GGCGTGGACG
551	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	GCGGCAAATA	A

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

m912.pcp

1 MKKSSLSISAL GIGILSIGMA FAAPADAVSQ IRQNATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTL LIR TYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI I KAK GVDGLIAELK AKNGGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng)
from *N. gonorrhoeae*:

g912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTILKSGDAASARPKAEAYAVP					
m912	: : : : : : : : : : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YFD F QRM TALAVGNPWRTASDAQQALAKEFQTLLIRTYSGTMLKFKNATVNVKDNPIVN					
m912	YFD F QRM TALAVGNPWRTASDAQQALAKEFQTLLIRTYSGTMLKLKNANVNVDNPIVN				:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGGKEIIVRAEVGIPGQKPVMNDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEEIKAK					
m912	: : : : : : : : : : : : : : :					
	130	140	150	160	170	180
	KGGKEIIVRAEVGVPGQKPVMNDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEEIKAK					

g912.pep 190 GIDGLIAELKAKNGGKX

m912

|:|||||||
 GVDGLIAELKAKNGGKX
 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq

1	ATGAAAAAA	CCTCCTTCAT	CAGCGCATTG	GGCATCGGTA	TTTTGAGCAT
51	CGGCATGGCA	TTTGCCGCC	CTGCCGACGC	GGTAAACCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	GCGGTGATGC	CAACACCGCC
151	CGCCAAAAAG	CCGAAGCCTA	TGCGATTCCC	TATTTTCGATT	TCCAACGTAT
201	GACCGCATTG	GCGGTGCGCA	ACCTTTGGCG	CACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAAGCGGC
451	GGTAAATACC	GTACCTACAA	CGTCGCCATC	GAAGGCGCGA	GCCTGGTTAC
501	CGTGTACCGC	AACCAATTCC	GCGAAATTAT	AAAGCGGAAA	GGCGTGGACG
551	GACTGATTGC	CGAGTTGAAG	GCTAAAAACG	GCAGCAAGTA	A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pap

1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQATQVLS ILKSGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFETTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI I KAK GVDGLIAELK AKNGSK*

m912/a912 98.0% identity in 196 aa overlap

		10	20	30	40	50	60
m912.pep		MKKSS	LISALGIGILSIGMAFAAPADAVSQIRQ	NATQVLSILKNGDANTARQKAEAYAIP			
			:	:	:	:	:
a912		MKKSSF	ISALGIGILSIGMAFAAPADAVNQIRQ	NATQVLSILKSGDANTARQKAEAYAIP			
		10	20	30	40	50	60
		70	80	90	100	110	120
m912.pep		YFDFQ	RM TALAVGNPWRTASDAQQALAKEFQTLLIR	ITYSGTMLKLKNANVNVKDNPIVN			
a912		YFDFQ	RM TALAVGNPWRTASDAQQALAKEFQTLLIR	ITYSGTMLKLKNANVNVKDNPIVN			
		70	80	90	100	110	120
		130	140	150	160	170	180
m912.pep		KGGKEI	IVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVT	VYRNQFGEIIKAK			
a912		KGGKEI	IVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVT	VYRNQFGEIIKAK			
		130	140	150	160	170	180
		190					
m912.pep		GVDGLIAELKAKNGGKX					
			:				
a912		GVDGLIAELKAKNGSKX					
		190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq

1	atGAAAAAA	CCGCTACGC	CATCCTCTG	CTGATCGGGT	TCGCTTCCGC
51	CCCTGCATTT	GCAGAAACC	GCCCCGCCGA	CCCTTATGAA	GGCTACAACC
101	GCGCCGTTTC	CAAATTC AAC	GACCAAGCCG	ACCGCTACAT	TTTCGCCCCCT
151	GCCGCGCGCG	GCTACCGCAA	AGTTACGCCG	AAACCCGTCC	GCGCCGGCGT
201	GTCCAATTTT	TTTAAACAAC	TGCGCGACGT	GGTCAGTTTC	GGCAGCAATA
251	TCTTGC GTTT	GcGacatCAA	cgcgcAAGcg	aAGACctcgT	CCGcgtcggc
301	atCAATACCA	CCTTCGGTTT	GGcgggGCTC	ATTGATATTG	CCGGcgcGGg
351	cggcggttccc	gacaataaaaa	AcacTttgGg	cgacacgttt	gctcggtGGG
401	GctgGAAAAa	cagcaATTAT	TTCGTgttgc	CCGtcttagg	cccgctccac

g913.pcp

m913.seq

m913 . pep

q913/m913

BNSDOCID: <WO 9957280A2 | >

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTC AAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGCACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AADKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVRAGVSNNFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVVRAGVSNNFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
a913						
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913						
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```
1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTCGGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCTGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTT TCGGGCGTGg tgTtttGcgC TTCGTGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG
```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```
1  MKKCILGILT ACAAMPADF RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMRVNIFIC SGVVFCASSR MMYAPLSVLP RI*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```
1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTCGGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCTGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTTCGTAGG CTTTCACGAT TTTTTCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTCGC CGTAATGAC GCGTTTCGCG CCGAAGCCGA TCGGGGTCAG
651 GAACATTTTC ATTTGTTTCG GCGTGTGTTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG
```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```
1  MKKCILGILT ACAAMPADF RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA
```

151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMRVNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLRLAQLHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLRLAQLHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETD-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRKFDXCIGWTDKETD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALECSQSCSADSXASTIFCTRGCRRTSSPVKWKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKWKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPNPDLMFLGRSIWLSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPNPDLMFLGRSIWLSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTGCG	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTGCGA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCGA	TTGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGGCA	TTGGAATGTC	AGTCGTGTTT	TGCCGATTCT
451	TAGGCTTCGA	CGATTTTTTG	CACCAAAGGA	TGCCGGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAGT	TTCTCACGCG
551	CATCTTTTAA	TCCCGATTGT	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCGTCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

1	MKKCILGILT	ACAAMPAFAD	RIGDLRLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCDEDA
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LECSQCSADS
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPNDL	MFLGRSIWLV
201	SPVMTAFAPK	PMRVNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*

m914/a914 98.4% identity in 244 aa overlap

```

      10      20      30      40      50      60
m914.pep  MKKCILGILTACAAMPAFADRIDGLEARLAQLEHRVAVLES GGNTVKIDLF GSNSTMYVC
          |||||
a914      MKKCILGILTACAAMPAFADRIDGLEARLAQLEHRVAVLES GSNSTVKIDLF GSNSTMYVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m914.pep  SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD
          |||||
a914      SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--
      70      80      90     100     110

      130     140     150     160     170     180
m914.pep  TELGFRICFSLPDFPCIGFQTALEQCSCSAD SXASTIFCTKGCRTTSSPVKVKYSPSTL
          |||||
a914      TELGFRICFSLPDFPCIGFQTALEQCSCSAD SXASTIFCTKGCRTTSSPVKVKYSPSTL
      120     130     140     150     160     170

      190     200     210     220     230     240
m914.pep  CSFSRASFNPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
          |||||
a914      CSFSRASFNPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
      180     190     200     210     220     230

m914.pep  LPRIX
          ||||
a914      LPRIX
          240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

```

g915.seq
1   ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gTTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

```

g915.pep
1   MKKTLLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAOIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGMGAEAD ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

```

m915.seq
1   ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

```

1  MKKTLAIVA VSALSXCRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
g915	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGGAEDALPFGNKEQA EKFAKDGGKVVGFDDMPDTYIFKX					
g915	GFIGGGAEDALPFGNKEQA EKFAKDGGKVVGFDDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

```

1  ATGAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

```

1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSXCRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac  atctgccact  cgcCGTCctg  actgctTtgc  tgcttgccagc
51  gtgcGGCGGT  Tcggacaaac  cgcctgccga  Aaaaccggca  ccggcgGaAA
101  accaaAacgt  atTgaAAATT  TataACTGGT  CGGAATACGT  CGATCCGGAA
151  ACCGTTGCCG  ATTTTGAAAA  GAAAAACGGC  ATCAAGGTTA  CTTATGATGT
201  GTACGACAGT  GATGAAACGC  TGGAAAGCAA  GGTGCTGACC  GGAAAATCCG
251  GTTACGACAT  TGTGCGCCCG  TCCAATGCGT  TTGTGGGCAG  GCAGATTAAG
301  GCAGGTGCGT  ATCAGAAAAT  CGATAAGTCG  ATGATTCCCA  ATTATAAACA
351  TCTCAACCCCT  GAAATGATGA  GGCTGATGGA  CGGGGTCGAT  CCCGACCACG
401  AATACGCCGT  GCCGTTTTAT  TGGGGGACAA  ATACCTTCGC  CATCAATACC
451  GAACGCGTGA  AAAAGGCTTT  GGTACGGAC  AAGCTGCCGG  ACAACCAAGT
501  GGATTTGGTG  TTCAACCCCG  AATACACGTT  CAAACTCAAA  CAATGCGGCA
551  TCAGCTATTT  GGACAGCGCG  GCGGAAATTT  ATCCCATGGT  GTTGAACAT
601  TTGGGCAAAA  ACCCGAACAG  CAGCAATACG  GAAGACATCA  GGGAGGCAAC
651  CGCCCTGCTC  AAGAAAAACC  GCCCAATAT  CAAACGCTTT  ACTTCGTCCG
701  GCTTTATCGA  TGATTTGGCG  CGCGGCGATA  CCTGCGTAAC  AATCGGTTTC
751  GCGGAGATT  TGAACATCGC  CAAACGCCGT  GCCGAAGAAG  CGGGCGGCAA
801  GGAAAAATC  CGCGTGATGA  TGCCGAAAGA  GGGCGTGGGG  ATTTGGGTGG
851  ATTCTTTCGT  GATTCCGAAA  GATGCGAAAA  ACGTCGCCAA  CGCGCACAAA
901  TACATCAACG  ACTTCCTCGA  TCCGGAAGTG  TCGGCGAAAA  ACGGCAATTT
951  cgttacCTAC  GCGCCTTCGA  GCAAGCCGGC  GCGCGATTTG  ATGGAGGACG
1001  AATTTAAAAA  CGACAATACG  ATTTTCCCGA  GCGGGGAAGA  TTTGAAAAAC
1051  AGCTTTATCA  TGGTGCCTAT  CCGGCCGGCG  GCATTGAAGT  TTATGGTGCG
1101  CCACTGGCAG  GATGTGAAGG  CGGGGAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL  TALLLAACGG  SDKPPAEKPA  PAENQNVLKI  YNWSEYVDPE
51  TVADFEKKNQ  IKVTYDVYDS  DETLESKVL  GKSGYDIVAP  SNAFVGRQIK
101  AGAYQKIDKS  MIPNYKHLNP  EMMRLMDGVD  PDHEYAVPFY  WGTNTFAINT
151  ERVKKALGTD  KLPDNQWDLV  FNPEYTFKLK  QCGISYLSA  AEIYPMVLNY
201  LGKNPNSSNT  EDIREATALL  KKNRPNIKRF  TSSGFIDDLA  RGDTCVTIGF
251  GGDINIARR  AEEAGGKEKI  RVMPKPEV  IWVDSFVIPK  DAKNVANAHK
301  YINDFLDPEV  SAKNGNFVTY  APSSKPARDL  MEDEFKNDNT  IFPSGEDLKN
351  SFIMVPIRPA  ALKFMVRQWQ  DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC  ATCTGCCCTT  GGCCGTCCTG  ACTGCTTTGC  TGCTTGCCAGC
51  GTGCGGCGGT  TCGGACAAAC  CGCCTGCCGA  AAAACCGGCA  CCGGCGGAAA
101  ACCAAAACGT  ATTGAAAATT  TACAACTGGT  CGGAATATGT  CGATCCGGAA
151  ACCGTTGCCG  ATTTTGAAAA  GAAAAACGGC  ATCAAGGTTA  CTTATGATGT
201  GTACGACAGC  GATGAAACGC  TGGAAAGCAA  GGTGCTGACA  GGCAAGTCCG
251  GTTACGACAT  TGTGCGCCCG  TCCAATGCGT  TTGTGGGCAG  GCAGATTAAG
301  GCAGGTGCGT  ATCAGAAAAT  CGATAAGTCG  CTGATTCCCA  ATTATAAACA
351  CCTCAACCCC  GAAATGATGA  GGCTGATGGA  CGGGGTCGAT  CCCGGCCACG
401  AATACGCCGT  GCCGTTTTAT  TGGGGGACAA  ATACCTTCGC  CATCAATACC
451  GAACGCGTGA  AAAAGGCTTT  GGTACGGAC  AAGCTGCCGG  ACAACCAAGT
501  GGATTTGGTG  TTCGACCCCG  AATACACGTC  CAAACTCAAG  CAATGCGGCA
551  TCAGCTATTT  GGACAGCGCG  GCGGAAATCT  ATCCTATGGT  GTTGAACAT
601  TTGGGTAAAA  ACCCGAACAG  CAGCAATACG  GAAGACATCA  GGGAGGCAAC
651  CGCCCTACTC  AAGAAAAACC  GCCCAATAT  CAAACGCTTT  ACTTCGTCCG
701  GCTTTATCGA  TGATTTGGCG  CGCGGCGATA  CCTGCGTAAC  AATCGGTTTC

```

751 GGC GCG GATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACCTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CAGTGGCAG GATGTGAAGG CGGGGAATA A

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCTVTIGF
251 GGD LNIARR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPA PAENQNVLKI YNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPA PAENQNVLKI YNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAP SNAFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAP SNAFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLSAAAEIYPMVLNLYLGKNPNSSNTEDI REATALLKKNRPNIKRF TSSGFIDDLA					
g917	QCGISYLSAAAEIYPMVLNLYLGKNPNSSNTEDI REATALLKKNRPNIKRF TSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

370

m917.pep ALKFMVRQWQDVKAGKX
|||||
g917 ALKFMVRQWQDVKAGKX
370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
1 ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAGC
51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAAATT TACAACGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCTG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTGGTG TTTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVLTKGSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKALGTD KLPDNQWDLV FDPEYTSKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPE TVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPE TVADFEKKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAP SNAFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAP SNAFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDNQWDLVFDPEYTSKLK					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDNQWDLVFDPEYTSKLK					
	130	140	150	160	170	180
m917.pep	QCGISYLSAAEYIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLSAAEYIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep						

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```

a917      QCGISYLDAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240
           250      260      270      280      290      300
m917.pep  RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           |||||
a917      RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300
           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVTYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||
a917      YINDFLDPEVSAKNGNFVTYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360
           370
m917.pep  ALKFMVRQWQDVKAGKX
           |||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGTCAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTTCAAAC CCCCCTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGCTAT TACGAACCG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCCTT CCCGATTAC GGTATTCCC ACGATTTTAT
501 CTCCGTCCC CTGCCTGCC GTTTCGCGG CGGAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGGAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCCG ACCTCTCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCCT
801 GAAAACCCCg tccggcaaat acatCCGCa cggTaagcc gacAAAAACG
851 AACatccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGVTGY YEPVLKGDGR
151 RTERARFPPI GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSLFPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAGS GNEGPGVAGL
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:
m919.pep

1	<u>MKKYLFRAAL</u>	<u>YGIAAAILAA</u>	<u>CQSKSIQTFP</u>	<u>QPDTSVINGP</u>	<u>DRPVGIPDPA</u>
51	<u>GTTVGGGGAV</u>	<u>YTVVPHLSLP</u>	<u>HWAAQDFAKS</u>	<u>LQSFRLGCAN</u>	<u>LKNRQGWQDV</u>
101	<u>CAQAFQTPVH</u>	<u>SFOAQOFFER</u>	<u>YFTPWQVAGN</u>	<u>GSLAGTVTGY</u>	<u>YEPVLKGDDR</u>
151	<u>RTAQARFPIY</u>	<u>GIPDDFISVP</u>	<u>LPAGLRSGKA</u>	<u>LVRIRQTGKN</u>	<u>SGTIDNTGGT</u>
201	<u>HTADLSRFFI</u>	<u>TARTTAIKGR</u>	<u>FEGSRFLPYH</u>	<u>TRNQINGGAL</u>	<u>DGKAPILGYA</u>
251	<u>EDPVELFMFH</u>	<u>IQSGRLKTP</u>	<u>SGKYIRIGYA</u>	<u>DKNEHPYVSI</u>	<u>GRYMADKGYL</u>
301	<u>KLQGTSMQGI</u>	<u>KSYMRQNPQR</u>	<u>LAEVLGQNPS</u>	<u>YIFFRELAGS</u>	<u>SDNGPVGALG</u>
351	<u>TPLMGEYAGA</u>	<u>VDRHYITLGA</u>	<u>PLFVATAHPV</u>	<u>TRKALNRLIM</u>	<u>AQDTGSAIKG</u>
401	<u>AVRVDYFWGY</u>	<u>GDEAGELAGK</u>	<u>QKTTGYVWQL</u>	<u>LPNGMKPEYR</u>	<u>P*</u>

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	: : : : : :					
g919	MKKHLLRSALYGIAAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAQOFFER					
	: : :					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAQRFFER					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNEGVPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	:					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

a919.seq

1	ATGAAAAAAT	ACCTATTCCG	CGCCGCCCTG	TGCGGCATCG	CCGCCGCCAT
51	CCTCGCCGCC	TGCCAAAGCA	AGAGCATCCA	AACCTTTCCG	CAACCCGACA
101	CATCCGTCAT	CAACGGCCCG	GACCGGCCGG	TCGGCATCCC	CGACCCGCC
151	GGAACGACGG	TCGGCGGCCG	CGGGCCGTT	TATACCGTTG	TGCCGCACCT
201	GTCCCTGCCC	CACTGGGCGG	CGCAGGATTT	CGCCAAAAGC	CTGCAATCCT
251	TCCGCCTCGG	CTGCGCCAAT	TTGAAAAACC	GCCAAGGCTG	GCAGGATGTG
301	TGCGCCCAAG	CCTTTCAAAC	CCCCGTCCAT	TCCGTTTCAGG	CAAAACAGTT
351	TTTTGAACGC	TATTTACAGC	CGTGGCAGGT	TGCAGGCAAC	GGAAGCCTTG
401	CCGGTACGGT	TACCGGCTAT	TACGAGCCGG	TGCTGAAGGG	CGACGACAGG
451	CGGACGGCAC	AAGCCCGCTT	CCCGATTTAC	GGTATTCCCG	ACGATTTTAT
501	CTCCGTCCCC	CTGCCTGCCG	GTTTGCGGAG	CGGAAAAGCC	CTTGTCGCA
551	TCAGGCAGAC	GGGAAAAAAC	AGCGGCACAA	TCGACAATAC	CGGCGGCACA
601	CATACGCCCG	ACCTCTCCCA	ATTCCCCATC	ACTGCGCGCA	CAACGCAAT
651	CAAAGGCAGG	TTTGAAGGAA	GCCGCTTCCT	CCCCTACCAC	ACGCGCAACC
701	AAATCAACGG	CGGCGCGCTT	GACGGCAAAG	CCCCGATACT	CGGTACGCC
751	GAAGACCCCG	TCGAACTTT	TTTTATGCAC	ATCCAAGGCT	CGGGCCGTCT
801	GAAAACCCCG	TCCGGCAAAT	ACATCCGCAT	CGGCTATGCC	GACAAAAACG
851	AACATCCCTA	CGTTTCCATC	GGACGCTATA	TGGCGGACAA	AGGCTACCTC
901	AAGCTCGGGC	AGACCTCGAT	GCAGGGCATC	AAAGCCTATA	TGCAGCAAAA
951	CCCACAACGC	CTCGCCGAAG	TTTTTGGGGCA	AAACCCAGC	TATATCTTTT
1001	TCCGAGAGCT	TACCGGAAGC	AGCAATGACG	GCCCTGTCCG	CGCACTGGGC
1051	ACGCCGCTGA	TGGGCGAGTA	CGCCGGCGCA	GTCGACCGGC	ACTACATTAC
1101	CTTGGGCGCG	CCCTTATTTG	TCGCCACCGC	CCATCCGGTT	ACCCGCAAGG

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```
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATT TTGGGGATAC GCGGACGAAG CCGGCGAAC
1251 TGCCGCAAA CAGAAAACCA CCGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCG CCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:
a919.pep

```
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQAQRFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMOGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*
```

m919/a919 98.6% identity in 441 aa overlap

m919.pep	10	20	30	40	50	60
a919	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
a919	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
a919	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
a919	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
a919	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
a919	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
a919	370	380	390	400	410	420
m919.pep	430	440				
a919	430	440				

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc  tggttaccga  aaaAGGTAAG  GAAAACATGA  TTCAACGCGG
51  CACATACAAC  TACCAATACC  GCAGCAACCG  TCCCGTCAAA  GACGGCAGCT
101 ACCTCGTTAC  CGCCGAATAT  CAGCCTACTT  TCCGGTCAAA  AAACAAAGCA
151 GGCTGGAAC  AGGCTGGCAT  CAAAGAAATG  CCTGACGCAA  GCTATTGCGA
201 ACAAACCCGT  ATGTTTCGTA  AAAACATTGT  CAACGTGGGA  CACGAAAGCG
251 CGGACACCGC  CATCATCACC  AAACCGGTCG  GACAAAACCT  GGAAATCGTC
301 CCGCTGGACA  ATCccgcccga  caTTCACgtg  ggctaacgCt  tcaaaGTccg
351 cgTtCtggtc  cgtGGCgaac  cgCTGcccaa  tgccACCgtt  accgCtacAT
401 TTGacggctt  cGAcaccagc  gaccgcagca  aaacgcacaa  Aaccgaagcc
451 caagcctTCT  ccgacaccac  cgacggcgaa  ggcgagtggt  acatcatCCC
501 CTTGCgccaa  GGCTTttgga  aAgcGAGTGT  CGAATAcaaa  gccgAttccc
551 CCGATcaaAG  CCTGTGccga  AAACagggcA  ACTACaCaac  TTtaaccttc
601 caaatcgccc  attctCacca  tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK  ENMIQRGTYN  YQYRSNRPVK  DGSYLVTAAY  QPTFRSKNKA
51  GWKQAGIKEM  PDASYCEQTR  MFGKNIVNVG  HESADTAIIT  KPVGQNLEIV
101 PLDNPADIHV  GXRFKVRVLF  RGEPLPNATV  TATFDGFDTS  DRSKTHKTEA
151 QAFSDTTDGE  GEVDIIPLRQ  GFWKASVEYK  ADFPDQSLCR  KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA  CATTGACACT  GCTCTCCGTT  TCCGCCCTAT  TTGCCACATC
51  CGCCACGCC  CACCGmGTCT  GGGTCGAAAC  CGCCACACG  CACGGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTTCCCGA  ACTCGAACCC
151 ATCGCCAAAG  ACCGCTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGC  AAGGAAACA  TGATTCAACG  CGGCACATAC  AACTACCACT
251 ACCGAAGCAA  CCGTCCCGTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA
301 TATCAGCCTA  CTTTCTGGTC  AAAAwACAAA  GCAGGCTGGA  AACAGGCGGG
351 CATCAAAGAA  ATGCCTGACG  CAAGCTATTG  CGAACAAACC  CGAATGTTTCG
401 GCAAAAACAT  CGTCAACGTC  GGACACGAAA  GCGCGGACAC  CGCCATCATC
451 ACCAArCCGG  TCGGACAAAA  CTTGGAAATC  GTCCCGCTGG  ACAATCCCGC
501 CAACATTCAC  GTAGGCGAAC  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551 AACCGCTGCC  CAATGCCACC  GTTACCGCCA  CCTTTGACGG  CTTGACACC
601 AGCGACCGCA  GCAAAACGCA  CAAwmCCGAA  GCACAGGCTT  TCTCCGACAG
651 CACAGACGAC  AAAGGCGAAG  TGGACATCAT  CmCCTTGCGC  CAAGGCTTCT
701 GGAAAGCCAA  TGTCGAACAC  AAAACCGACT  TCCCCGATCA  AAGCGTGTGC
751 CAAAAACAGG  CGAACTACTC  GACTTTAACC  TTCCAAATCG  GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV  SALFATSAHA  HRVWVETAHT  HGGEYLKADL  GYGEFPELEP
51  IAKDRLHIFS  KPMQLVTEKG  KENMIQRGTY  NYQYRSNRPV  KDGSYLVIAE
101 YQPTFWSKKK  AGWKQAGIKE  MPDASYCEQT  RMFGKNIVNV  GHESADTAII
151 TKPVGQNLEI  VPLDNPANIH  VGERFKVRVL  FRGEPLPNAT  VTATFDGFDT
```

g920/m920

```

g920.pep          10          20          30
                  PMQLVTEKGKKNMIQRGTYNQYRSNRPVK
                  |||||
m920              GGEYLKADLGYGFEPELEPIAKDRLHIFSKPMQLVTEKGKKNMIQRGTYNQYRSNRPVK
                  40          50          60          70          80          90
                  40          50          60          70          80          90
g920.pep          DGSYLVTAEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
                  |||||
m920              DGSYLVIAEYQPTFWSKKKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
                  100         110         120         130         140         150
                  100         110         120         130         140         150
g920.pep          KPVGQNLEIVPLDNPADIHVGXRFKVRVLFERGEPLPNATVTATFDGFDTSDRSKTHKTEA
                  |||||
m920              KPVGQNLEIVPLDNPANIHVGERFKVRVLFERGEPLPNATVTATFDGFDTSDRSKTHXXEA
                  160         170         180         190         200         210
                  160         170         180         190         200
g920.pep          QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRKQANYTTLTFQIAHSHHX
                  |||||
m920              QAFSDSTDDKGEVDIIIXLRQGFWKANVEHKTDFPDQSVCKQANYSTLTFQIGHSHHX
                  220         230         240         250         260

```

```

a920.seq
1  TGAAGAGAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCGCATC
51  CGCCCCACGC  CACCCGCTCT  GGGTCGAAAC  CGCCCCACAG  CACGGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AAATTTCCCGA  ACTCGAACC
151 ATCGCCAAAG  ACCGCTTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGC  AAGGAAAAACA  TGATTCAACG  CGGCACATAC  AACTACCACT
251 ACCGAAGCAA  CCGTCCCGTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA
301 TATCAGCCTA  CTTTCTGGTC  AAAAAACAAA  CGAGGCTGAA  AACAGGCGGG
351 CATCAAAACA  ATGCTTGAGC  CAAGCTATTG  GCAGCAAAAC  CGAATGTTCT
401 GCAAAAACAT  CGTCAACGTC  GGACACGAAA  GCGCGGACAC  CGCCATCATC
451 ACCAAACCGG  TCGGACAAAA  CTTGGAAATC  GTCCCGCTGG  ACAATCCCGC
501 CAACATTAC  GTAGGCGAAC  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551 AACCGTGC  ATGTCACACC  GTTACCGCCA  CCTTTGACGG  CTTCCGACAC
601 AGCGACCGCA  GCAAAACGCA  CAAAACCGAA  GCACAGGCTT  TCCGACAG
651 CACAGACGAC  AAAGGCGAAG  TGGACATCAT  CCCCTTGCGC  CAAGGCTTCT
701 GGAAAGCCAA  TGTCGAACAC  AAAGCCGACT  TCCCGATCA  AAGCGTGTGC
751 CAAAAACAGG  CGAACTACTC  GACTTTAACC  TTCCAAATCG  GCCATTGCA
801 CCATTAA

```

a920.ppep

1	<u>*KKTLLTLLAV</u>	<u>SALFAASAHA</u>	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRLHIFS	KPMQLVSTEK	KENMIQRGTY	RMQYRSNRVP	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	NYFGKNIVNV	GHSADTAII
151	TKPVGQNL EI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFD T
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	QKQANYSTLT	FOIGHSHH*			

BNSDOCID: <WO_9857280A2_|>

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	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFFPELEPIAKDRLHIFS					
a920	XKKTLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGEFFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAEYQPTFWSKXKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXHEAQAFSDSTDDKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQKQANYSTLTTFQIGHSHHX					
a920	KADFPDQSVQCQKQANYSTLTTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1 ATGAAGAAAA CATTGACACT GCTCGCcggt TcCGCACTAT TTGCCACATc
51 cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCGTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTTCG
401 GTAAAAACAT TGTCACCGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG TAGGCGGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGGCG CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1 MKKTLTLLAV SALFATSAHP HRVWVETAHT HGGEYLKADL GYGEFFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 KQQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1 ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACAG CACGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCGTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATA AACTACCAAT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GTCATTCGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 KQQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTD KGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDT D KGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFFDQSVCKQKQANYSTLTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAGAAGAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAGGCG AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

a920.pep

```

1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*
```

m920-1/a920 98.9% identity in 267 aa overlap

```

      10      20      30      40      50      60
m920-1.pep  MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          |||
a920        XKKTLTLLAVSALFAASAHAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
      10      20      30      40      50      60

      70      80      90     100     110     120
m920-1.pep  KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIIEYQPTFWSKNKAGWKQAGIKE
          |||
a920        KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIIEYQPTFWSKNKAGWKQAGIKQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m920-1.pep  MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
          |||
a920        MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m920-1.pep  FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
          |||
a920        FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
      190     200     210     220     230     240

      250     260     269
m920-1.pep  KTDFFPDQSVCKQKQANYSTLTFFQIGHSHHX
          |||
a920        KADFFPDQSVCKQKQANYSTLTFFQIGHSHHX
      250     260
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

g921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatccccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCGG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

g921.pep

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAMD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

m921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

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251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAVDSQGEINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	: :					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATGACGGA AATCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAG GTTCCGCCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSI VAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTTGTG GACGATGAAG TCGGGAAAGG GGATTTTTC CAGGCGGAAT
251 GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301 ATGCACCGAC CCTCCACATC GCGTCCGTGG TATgtgttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcgggttat cgatgatgtg gcgCAAAAat acggcgGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCCAAAAA GAATTGGTTC AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTATATC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTAtat gaagCAGCAC GGTGGCGCA CgggcggTAA
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CAggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATT GAaggCGTAc
901 ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTTGTT
951 CAAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTG GGCTTGAACA
1001 ATTTTATATC GGTATGGCAG TACAACCACA GCCGATGTA TGTAAACGgcg
1051 gtcaggGACA TTGCCAATTC GCTCGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFRGTNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFY YPRRAGFFOK ELVELLKLAK
201 EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTTGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATTT CGGGCAAGGC GAAATTTTCG GCAGCGCGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATCTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG CCGGGTTTT TCAAAAAGA ATGGTTCGAG

```


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```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGGC GATGTTTTTCG CCTTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GCGGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACCGGGC GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTTCG TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1  MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEGG DVFAFKGSYA GAMGMPQFMP SSKRWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

```

m922.pep      10      20      30      40      50      60
               MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP
g922           10      20      30      40      50
               MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPAFDAA-----AVP

m922.pep      70      80      90      100     110     120
               VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
g922           60      70      80      90     100     110
               VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAYKADIVKIMHRPSTSRPWYVFR

m922.pep     130     140     150     160     170     180
               TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL
g922          120     130     140     150     160     170
               TGNSGRAKPHGARRFYAENRAVIDDVAQKYGVPaelivaiIGIETNYGKNTGSFRVADAL

m922.pep     190     200     210     220     230     240
               ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
g922          180     190     200     210     220     230
               ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY

m922.pep     250     260     270     280     290     300
               DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV
g922          240     250     260     270     280     290
               DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV

m922.pep     310     320     330     340     350     360
               ADLKAYGIIPGEELADDEKAVL FKL ETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
g922          310     320     330     340     350     360
               ADLKAYGIIPGETLADDEKAVL FKL ETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI

```

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	300	310	320	330	340	350
		370				
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTCCGC ACGGGAATT CGGGCAAGGC GAAATTTCCG GCGCGCGGCC
401 GGTTTTATGC GGAAACCCTG CCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGGTTT TCCAAAAAGA ATTGCTGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTTAAAGG
651 CAGCTATGCG GGCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGC ATGTCGCGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GGCGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAAAGCG GTTTTGTTC AACTGGAAAC CGCACCCGCG GTGTTTGAAT
1001 ATTATTTGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWRT GSKILVSATL APGADVQAI GEKALTTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKESRPAFDAAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMCKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGKGKMLVSATLAPGADVQAIIGEKALTRTV
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANANYMKQHGWRGKGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          ||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAACACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAACGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRITVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAACGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTCGCCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPRHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRITVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPPF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

```

      10      20      30      40      50      60
g923.pep  MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL
          |||||  |||||  |||||  |||||  |||||  |||||
m923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL
          10      20      30      40      50      60

      70      80      90      100
g923.pep  LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLLTVSGNVLATCILID-----
          |||||  |||||  |||||  |||||  |||||  |||||
m923      LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS
          70      80      90      100      110      120

      110      120
g923.pep  -----YFVPPELFFVKLGQHLX
          |||||  |||||  |||||  |||||
m923      PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX
          130      140      150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

```

a923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTCT
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CTTGTTCGG
201 CGGTTGGGCG GCGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAGCG TTTTGTGTGT CTGTCCGTC TGA CTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGTCTGCGG CTTCTGCGC
451 TTGTCTGAT TTTTGTTAAT CCACTAT.AT TATTTGTCC CGCCTGAATT
501 TTTCGTAAA CTGCGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

```

a923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLEYAFAL YGIDKRRRAVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFVV LFRLTVSGNV
101 LATLILIIYS LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

```

      10      20      30      40      50      60
m923.pep  MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL
          |||||  |||||  |||||  |||||  |||||  |||||
a923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL
          10      20      30      40      50      60

      70      80      90      100      110      120
m923.pep  LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS
          |||||  |||||  |||||  |||||  |||||  |||||
a923      LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS
          70      80      90      100      110      120

      130      140      150      159
m923.pep  PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX
          |
a923      PXAQRERFSKVLKHQVNRFR TICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX
          130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcgcggtgt TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgaggggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTCACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
	:				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTCACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKOMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51 KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAAGCAA TTAATTCCTT
151 AATAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKOMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTKGE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKOMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGE					
g925-1	MKOMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYQQRQAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAATCA ACGTGTTTAC AGGTAAGGAA GAATCTATGC TTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTATG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGEESMLLSEKDGALSINTGIGE			
	30	40	50	60
	40	50	60	70
				80
				90

```

a925-1.pep  IPIKLSDDGKELYVERROYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERROYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

g926.seq (partial)

```

1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCCTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTCA GCGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

g926.pep (partial)

```

1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

m926.seq

```

1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCCTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

m926.pep

```

1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWTVGR
151 ADSSGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEQTEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEQSAEELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRWGASPNVATE

```

|||||
m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
130 140 150 160 170 180

a926.seq

```

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACCC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATAAGT AA

```

a926.pep

```

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSSGQVRTL QLNNGNLNIIR LVFTEIGMPS ETETQECCAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEGKGSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQESAELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQESAELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQECCARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

```

1 atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51 CAGCCCcgca GCcgatTcaa accaTCCGTC CGGACAAaAT GCCCCGCGCA
101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTegtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTgtgttg tcggaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCAGGCC GCACCCTACA

```



```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgc
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAActCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGA AACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTYSQE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
201 LKNTVPFENG GRXPPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAT GCCCCGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAAGAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GcKcGCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGAAAA
701 CGAAGCCAAC TACGTCAGCr AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

```

          10      20      30      40      50      60
g927.pep  MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD
          |||||
m927       MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

          70      80      90      100     110     120
g927.pep  HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK
          ||: |||||
m927       PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

          130     140     150     160     170
g927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNGRYAFLGA
          |||||
m927       GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA
          130     140     150     160     170     180

```

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTVPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS
          |||||::|||
m927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          |||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
  1  ATGAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAAA  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
  1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

m927.pep KNX
 |||
a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51 CGCCTGGTT TTGGCACTGC CCGTACcga CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAacgctggg CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCcgat TATGCagtcg attgCcggCA GttacggctC
501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
551 tcaattatCA TTCaaTCCC atttcgctcg ctAtggctat taCTGcaact
601 gCCCCcaacc CTTAATcgt caacttgatt gccGaaaaTt taggcagtag
651 tttccgctCTT Tcttgggggg cgTGGGcgtg ggcaatGGCT Gttcccgcg
701 ttatcgctt TTtctgTTATG CCTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCTgttCAA TTTGCCAAAG ACCGTCTGAG
801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGG AAAGAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTtaAATA Aactcggact gattaaatGG TTCTCCGGAG TGTGGCGGA
1101 Aagtgtcggc GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCCGGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGGG TGGAAAGTTC
1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMP VGVIAAIIGK
51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNVAV FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51 CGCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCGATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

451  GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501  CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551  TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601  GCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651  TTCCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701  TTATCGCCTT TTTCTGTATG CCTTTGATT TATATTTwyT GTATCCGCCT
751  GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801  GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851  GTATCTTGCT GCTGTGTGG GCAGATGTT CCGCCCTTAT TACCGGCAAT
901  CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951  GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAATGG TTCTCCGGAG TGTTGGCGGA
1101 AAGTGTGGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTTTCGCT GCTGCCGTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTFA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMCKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK VMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK AMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMCKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMCKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNSNPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSNPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADVPAITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPAITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCACT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTTGGCGGA
1101 AAGTCTCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```
a929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIIVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*
```

m929/a929 99.6% identity in 487 aa overlap

```

      10      20      30      40      50      60
m929.pep  MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII
          |||
a929      MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m929.pep  AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIIVMISRGLLKTGLGMRI
          |||
a929      AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIIVMISRGLLKTGLGMRI
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m929.pep  FGRKTLGIGYSLALSELLLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
          |||
a929      FGRKTLGIGYSLALSELLLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
m929.pep  LALVNYHNSNPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
          |||
a929      LALVNYHNSNPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
          |||
      190     200     210     220     230     240

      250     260     270     280     290     300
m929.pep  PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV
          |||
a929      PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV
          |||
      250     260     270     280     290     300

      310     320     330     340     350     360
m929.pep  HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
          |||
a929      HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
          |||
      310     320     330     340     350     360

      370     380     390     400     410     420
m929.pep  FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAVSLNAPAM
          |||
a929      FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAVSLNAPAM
          |||
      370     380     390     400     410     420

      430     440     450     460     470     480
m929.pep  PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
          |||
a929      PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
          |||
      430     440     450     460     470     480

m929.pep  WKVLGYWX
          |||
```

a929

WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAATGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNP AEIRM QODIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWWLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCCGTAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAAG
201 ACGTATTGCA GCATTCCAAA ACAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGGAA CAAGGACTGG AAAATCTCAA ATGCTCCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCCGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACC ACAGGTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTATTTC GTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETksYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FGEGTSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGO IKLGGNLHYD

```

451 IFTGRALKKP EYFQTKKWVT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAAGTGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTT CCACCCGCTC GAACGATCTG
601 TTGAATCTGT GTGATTGGGA ACAAGGACTG GAAAATCTCA AACGCTCTCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTG GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAAT TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAATGGGA CATGGGCATT CAATCAACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAGAGTT
1151 ACATTGATGA TGCCGAACCTG ACTGTACAAC GCGGTAAACG TCGGGTGTGG
1201 TTGGCAGAAC TTTCCACAAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAT TGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAACAGC TATTTGCCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCTGCTA ACATCGCAAG
1451 ACAAACCTGG TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGTTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACCGGGGCA GATAAAGCTT GCGGCAACG TGCATTACGA
1701 TATATTTACC GGCCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGGCAAG CGGTTTTAG GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```
1 MKLPLSYLPN IRLSWCCLL AGIIPATLL ASPNPAEIRM QQDIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAGF NKFPTRSNL
201 LNLRLDLEQL ENLKRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHOAVSG LSEVDYNGK
351 SYNTDFGNR LLYRDAKRKT YLGVLWMRE TKSYYDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFLK YKRGTGMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWE WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

```
90      100      110      120      130      140
m930-1.pep AINEVVLEGEHHRFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI
g930-1.pep                               GKCLHAGDINQIMSLAQNALIGRGYTTTRI
                                         10      20      30

150      160      170      180      190      200
m930-1.pep LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAGFQNKFPTRSNLNLRLDLE
g930-1.pep LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAGFQNKFPTRSNLNLRLDLE
                     40      50      60      70      80      90

210      220      230      240      250      260
m930-1.pep QGLENLKRRLPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDSNGSEATGKYQG
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


1343

```

g930-1.pep  QGLENLKLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDNGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDNGKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270

m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  AELTVQRRKTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALARPEEAFGEGTSRMKI
              280      290      300      310      320      330

m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVRGFDGEMSLSAER
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVRGFDGEMSLPAER
              340      350      360      370      380      390

m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLAGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450

m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYYTF
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  IFTGRALKKPEYFQTKKWTGFGVGYSTFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTGCG GTTGTGTCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCC TTTCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMT DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
  1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
 51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101  ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151  TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201  CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251  CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301  AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351  CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401  ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451  ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501  TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTC
551  GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep.
  1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101  KNTAGTIAMA RTTAPDSATS OFFINLADXX SLDYKNGQYG YTVFGRVESG
151  MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLDESKASKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
g931.pep	OFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVFPVQPVKIRR					
m931	OFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVFPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
  1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
 51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101  ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151  TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201  CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251  CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301  AAAAACA CTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351  CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401  ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```

1345

451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVGQ*

m931/a931 94.6% identity in 185 aa overlap

m931.pep	10	20	30	40	50	60
	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
m931.pep	70	80	90	100	110	120
	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
m931.pep	130	140	150	160	170	180
	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVGQX					
a931	VVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTTC CACTCACCGC

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```

51  CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCGCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAa9g
551 cggtaaaCCC GGCGCTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1  MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQOGFEHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1  ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51  ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCG TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GCGCGGCGCG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAATTCAC ACGGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGACAGCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTnT GCATTGTGTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1  ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51  TGXRRAAVYL RPIDRKLAAA KPGRRGRRV YRQAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQOG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

m934.pep          10          20          30
                  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
g934              10          20          30          40          50          60
                  MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI

m934.pep          40          50          60          70          80          90
                  PAEAQANGNNGQPVTKXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
g934              70          80          90          100         110         120
                  PAQAQANGNNGQPVTKRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQAGKQIHTGGQPR

                  100         110         120         130         140         150

```

1347

```

m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPPRYARF
           ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
g934      QPRRPSRACCLPSVRTPQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPSRYARF
           130      140      150      160      170      180

           160      170      180      190      200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
           ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
g934      RQKAVNPARQCRLKGFQTAFLLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2869>:

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCAG
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGC GCGGTTT CCGCAGAAGG
551 CGGTAAATCC GCGGTGCCAA TGCGGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTGGGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2870; ORF 934.a>:

```

a934.pep
1  MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAEAQANGNN GQPVTX*RRR AVYLRPIDRK LAAAKPGRRG
101 GRRVYRQAG KQIHTGRQPR QSRRLPARACR LPSVRTSQCA HQQGFHAQF
151 PCKTTGGAGA ALPPDNAPAR QLPPPRHARF RQKAVNPACQ CRLKGFQTAF
201 LYLGLTLLCC RLIFRRHFVS KSLMSGWQF*

```

m934/a934 94.1% identity in 205 aa overlap

```

m934.pep  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
           ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
a934      MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
           10      20      30      40      50      60

           40      50      60      70      80      90
m934.pep  PAEAQANGNNGQPVTXRRRAAVYLRPIDRKLAAAKPGRRGGRRVYRQAGKQIHTGRQPR
           ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
a934      PAEAQANGNNGQPVTXRRRAAVYLRPIDRKLAAAKPGRRGGRRVYRQAGKQIHTGRQPR
           70      80      90      100     110     120

           100     110     120     130     140     150
m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPPRYARF
           ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
a934      QSRRLPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
           130     140     150     160     170     180

           160     170     180     190     200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
           ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
a934      RQKAVNPACQRLKGFQTAFLLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
           190     200     210     220     230

```

g935.seq not found yet

1349

```
601 AATAGAAATG CCAATAATGC CGCGCCGCG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCCGGGCGGA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AAAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGCTG
1251 GGCGCAGGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTGC
1501 GCGGATTGGC GGTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```
a935.pep
1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAEF
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*
```

m935/a935 98.8% identity in 505 aa overlap

```
10 20 30 40 50 60
m935.pep MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV
|||||
a935 MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV
10 20 30 40 50 60

70 80 90 100 110 120
m935.pep DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP
|||||
a935 DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP
70 80 90 100 110 120

130 140 150 160 170 180
m935.pep AEAVARYRELHGENAADERILLDLAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF
|||||
a935 AEAVARYRELHGENAADERILLDLAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF
130 140 150 160 170 180

190 200 210 220 230 240
m935.pep RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK
|||
a935 RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK
190 200 210 220 230 240

250 260 270 280 290 300
m935.pep LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS
|||
a935 LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS
250 260 270 280 290 300
```